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US-10-047-264A-4
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LENGTH: 263
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1218
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Sequence 28, Appl
Sequence 42, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 14, Appli
Sequence 114, Appl
                                                                                                                                                                                                 December 12, 2003, 12:14:52 ; Search time 48.1424 Seconds (without alignments) 1016.022 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                        1 MMPKHCFLGFLISFFLTGVA.......YQPMLDRRSQRSEERCVEIP 263
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(cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
(cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
(cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
(cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
(cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
(cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
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(cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
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(cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
(cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
(cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
(cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-09-949-192-6

US-09-961-404-4

US-10-237-496-114

US-10-242-505-114

US-10-243-5114

US-10-243-251-114

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US-10-243-251-114
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US-10-293-832-28
US-10-312-088-42
US-09-961-404-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           684280 segs, 185983659 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published_Applications AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1432
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Match Length DB
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No.
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16 1218 85.1 231 12 US-10-245-164-114 Sequence 31, Appl 18 1218 85.1 231 12 US-0-047-264A-2 Sequence 33, Appl 20 1218 85.1 231 12 US-10-047-264A-3 Sequence 35, Appl 21 12 US-10-047-264A-3 Sequence 35, Appl 22 12 US-10-047-264A-3 Sequence 31, Appl 22 12 US-10-244-972-114 Sequence 114, Appl 22 12 US-10-249-2114 Sequence 114, Appl 22 12 US-10-249-2114 Sequence 114, Appl 24 1218 85.1 231 12 US-10-249-214 Sequence 114, Appl 25 12 US-10-249-214 Sequence 114, Appl 26 1218 85.1 231 12 US-10-245-103-114 Sequence 114, Appl 27 12 US-10-245-103-114 Sequence 114, Appl 27 12 US-10-245-103-114 Sequence 114, Appl 29 12 US-10-245-103-114 Sequence 114, Appl 20 US-10-243-103-114 Sequence 114, Appl 20 US-10-243-103-114 Sequence 114, Appl 20 US-10-243-103-114 Sequence 114, Appl 20
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ALIGNMENTS

BEST AVAILABLE COPY

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61 FVQYKIMPSCSWKSSHQKPSGCWQHISCNFPGCRTLAKYĞQRQWKNKEDCWGTQELSCDL 120
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APPLICANT: Strum, Jay C.
APPLICANT: Xiang, Zhaoying
APPLICANT: Xie, Qing
APPLICANT: Rie, Qing
APPLICANT: Rie, Qing
APPLICANT: Rie, Qing
APPLICANT: Rie, Qing
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFRENCE: OF50029
CURRENT APPLICATION NUMBER: US/10/312,088
CURRENT FILING DATE: 2002-12-20
PRIOR PELING DATE: 2001-06-22
PRIOR FILING DATE: 2001-06-22
PRIOR PLING DATE: 2000-06-22
PRIOR PLING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PESESEQ for Windows Version 4.0
SEQ ID NO 42
LENGTH: 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 263; Conservative
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US-10-312-088-42
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Publication No. US20030180752A1.
Fublication No. US20030180752A1.
GENERAL INFORMATION:
APPLICANT: Liu, Wei
APPLICANT: Fouser, Lynette
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: TYPE 2 CYTOKINE RECEPTOR AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 22058-546
CURRENT APPLICATION NUMBER: US/10/293,832
CURRENT FILING DATE: 2002-11-12
FRIOR APPLICATION NUMBER: US 60/332,366
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.2
SEQ ID NOS: 33
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                                          PNLPYRYQKEKNVSIEDYYBLLYRVPIINNSLEKEQKVYEGAHRAVBIEALTPHSSYCVV 240
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llarity 100.0%; Pred. No. 4e-138;
Conservative 0; Mismatches 0
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Best Local Similarity
Matches 263; Conserva
                                                                                                                                                                                                                                                                                    RESULT 2
US-10-293-832-28
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0; Indels

; Pred. No. 4e-138; 0; Mismatches 0

100.0%; Score 1432; 100.0%; Pred. No. 4e

DB 12; Length 263;

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             Sequence 6, Application US/09961404

Sequence 6, Application US/09961404

Publication No. US20030022827A1

GENERAL INFORMATION:

APPLICANT: WEISS, BEXTRAM

APPLICANT: ASADULLAH, KHUSRU

APPLICANT: TOSCHI, LUISELIA

TITLE OF INVENTION: PAMILY CLASS 2

FILE REFERENCE: SCH-1788

CURRENT APPLICATION NUMBER: US/09/961,404

CURRENT FILLING DATE: 2001-09-25

NUMBER OF SEQ ID NOS: 19
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Best Local Similarity 99.6%; Pred. No. 1e-137;
Matches 262; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 263
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
US-09-961-404-6
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; Sequence 42, Application US/10312088; Publication No. US20030219862A1; GENERAL INFORMATION:

US-10-312-088-42

APPLICANT: Agarwal, Pankaj
APPLICANT: Cogswell, John P.
APPLICANT: Kabnic, Karen S.
APPLICANT: Lai, Ying-Ta
APPLICANT: Martensen, Shelby A.
APPLICANT: Murdock, Paul R.
APPLICANT: Smith, Randall F.

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61 FVQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDL 120
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                                                                                                                                                                    APPLICANT: Arai, Macko

APPLICANT: Sana, Theodore R.

APPLICANT: Sana, Theodore R.

APPLICANT: Mutphy, Exin E.

APPLICANT: Mutphy, Exin E.

APPLICANT: Savkoor, Chetan

APPLICANT: Savkoor, Chetan

APPLICANT: Savkoor, Chetan

APPLICANT: Sanith, Kathlen M.

APPLICANT: Smith, Kathlen M.

APPLICANT: McClanahan, Terrill K.

TITLE OF INVENTION: MadMaLIAN GENES; RELATED REAGENTS AND METHODS

FILE REFERENCE: DX01168K

CURRENT APPLICATION NUMBER: US/09/949,192

CURRENT PILICAN DATE: 2001-09-07

PRIOR APPLICATION NUMBER: 60/231,267

PRIOR APPLICATION NUMBER: 60/231,267

PRIOR PRIOR PLING DATE: 2000-09-08

SOFTWARE: Patentin version 3.1

SEQ ID NO 6

LENGTH: 231
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| Sequence 4, Application US/09961404
| Publication No. US20030022827A1
| GENERAL INFORMATION:
| APPLICANT: WEISA; BERTRAM
| APPLICANT: SABAT, ROBERT
| APPLICANT: ASADULLAH, KHUSRU
| APPLICANT: TOSCHI, LUISELLA
| TITLE OF INVENTION: FAMILY CLASS 2
| FILE REFERENCE: SCH-1788
| CURRENT APPLICATION NUMBER: US/09/961,404
| CURRENT APPLICATION NUMBER: US/09/961,404
| CURRENT FILING DATE: 2001-09-25
| NUMBER OF SEQ ID NOS: 19
| SOFTWARE: PatentIn Ver: 2.1
| SEQ ID NO 4
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                                              Sequence 6, Application US/09949192
Patent No. US20020142292A1
GENERAL INFORMATION:
                                                                                                          APPLICANT: Parham, Christi L. APPLICANT: Gorman, Daniel L. APPLICANT: Kurata, Hirokazu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 87.8
Matches 231, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-949-192-6
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                                                                                                                                                                  TSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHA 180
                                                                                                            61 FVQXKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWRNKBDCWGTQBLSCDL 120
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                           PNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVV
MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09728911
Sequence 2, Application US/09728911
GENERAL INFORMATION:
APPLICANT: Presentl, Scott R.
APPLICANT: Ku, Wenfeng
APPLICANT: Kindevogel, Wayne
TITLE OF INVENTION: Human Cytokine Receptor
FILE REFERENCE: 99-93
FILE REFERENCE: 99-93
FILE REFERENCE: 99-93
FILE REFERENCE: 99-93
FILE REPRENCE: 99-12-01
PRIOR APPLICATION NUMBER: US 60/169,049
PRIOR APPLICATION NUMBER: US 60/169,049
PRIOR APPLICATION NUMBER: US 60/232,219
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-10-31
PRIOR FILING DATE: 2000-10-31
SEOFTWARE PRIOR FILING SATE: 3000-10-31
NUMBER OF SEQ ID NOS: 36
SOFTWARE FASTESCQ FOR WINDOWS VERSION 3.0
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Best Local Similarity 87.83
Matches 231; Conservative
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ORGANISM: Homo sapiens
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US-09-728-911-2
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME TITLE OF INVENTION: ACIDS ENCODING THE SAME TITLE OF INVENTION: ACIDS ENCODING THE SAME CURRENT APPLICATION NUMBER: US/10/242,074 CURRENT FILING DATE: 2002-09-11 PRIOR APPLICATION NUMBER: US/197942 PRIOR FILING DATE: 2002-07-18 PRIOR FILING DATE: 1997-09-17 PRIOR PILING DATE: 1997-09-17 PRIOR PILING DATE: 1997-09-17 PRIOR PILING DATE: 1997-10-24 PRIOR PILING DATE: 1997-11-10 PRIOR APPLICATION NUMBER: 60/065027 PRIOR PILING DATE: 1997-11-10 PRIOR APPLICATION NUMBER: 60/065027 PRIOR PILING DATE: 1997-11-10 PRIOR PILING DATE: 1999-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHA 180
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                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                   Indels 32;
                                                                                                                                                    Length 231;
                                                                                                                                                 Query Match 85.1%; Score 1218; DB 12; Best Local Similarity 87.8%; Pred. No. 2.6e-116; Matches 231; Conservative 0; Mismatches 0;
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Publication No. US20030138897A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60,087607
PRIOR FILING DATE: 1000
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
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PRIOR FILING DATE: 1998-05-22
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Stephan, Jean-Phillippe
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; SEQ ID NO 114
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-237-496-114
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Fong, Sherman
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APPLICANT:
APPLICANT:
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APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watanbe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Pong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C4
                                                                                                                                                    Gaps
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NUMBER OF SEQ ID NOS: 116
                                                                                                                                                 32;
                                                                                                Length 231;
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                                                                                                DB 11;
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                                                                                             Query Match

85.1%; Score 1218; DB 11;
Best Local Similarity 87.8%; Pred. No. 2.6e-116;
Matches 231; Conservative 0; Mismatches 0;
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CURRENT FILING DATE: 2002-09-06
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PRIOR APPLICATION NUMBER: 10/197942
PRIOR APPLICATION NUMBER: 10/197942
PRIOR PLING DATE: 2002-07-18
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-24
PRIOR PLING DATE: 1997-10-24
PRIOR PLING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/065027
PRIOR PLING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/086478
PRIOR PLING DATE: 1998-05-22
PRIOR PLING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/080601
PRIOR APPLICATION NUMBER: 60/08061
PRIOR PLING DATE: 1998-06-18
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Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
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Publication No. US20030138896A1
GENERAL INPORMATION:
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PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
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Filvaroff, Ellen
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-404-4
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Query Match
Best Local Similarity 87.8
Matches 231; Conservative
                                                                                                                            TYPE: PRT
; ORGANISM: Homo Sapien
US-10-242-505-114
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APPLICANT:
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APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDE ENCODING THE SAME
FILE REFERENCE: P3630R1C25
                                                                                                                                                                                                                                                       1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY
Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 116 SEQ ID NO 114 LENGTH: 231
                                                                                                                                                                                                                 32;
                                                                                                                                                                       Length 231;
                                                                                                                                                                                                               Indels
                                                                                                                                                                  Query Match 85.1%; Score 1218; DB 12;
Best Local Similarity 87.8%; Pred. No. 2.6e-116;
Matches 231; Conservative 0; Mismatches 0;
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CURRENT PELLOATION NUMBER: US/10/242,505
CURRENT FILING DATE: 2002-09-11
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR PILING DATE: 2002-07-18
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-01-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/05699
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/09699
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR APPLICATION NUMBER: 60/089801
PRIOR APPLICATION NUMBER: 60/089801
PRIOR PILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
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Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
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Publication No. US20030138898A1
GENERAL INFORMATION:
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Filvaroff, Ellen
                                                                                                    ORGANISM: Homo Sapien
US-10-242-074-114
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APPLICANT: Smith, Victoria
APPLICANT: Scphan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watanbok_Colin
APPLICANT: Wood, William
APPLICANT: Pong, Sharman
APPLICANT: Zhang, Zemin
APPLICANT: Pong, Sharman
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE RFEREMENT APPLICATION NUMBER: US/10/242, 574
CURRENT APPLICATION NUMBER: US/10/197942
PRIOR APPLICATION NUMBER: 60/059114
PRIOR PILING DATE: 2002-07-18
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/065027
PRIOR APPLICATION NUMBER: 60/065027
PRIOR PILING DATE: 1998-05-22
PRIOR PILING DATE: 1998-05-22
PRIOR PILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-18
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PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 114
LENGTH: 231
                                                                                                                                                                                                                                                                  Length 231;
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                                                                                                                                                                                                                                                               85.1%; Score 1218; DB 12;
87.8%; Pred. No. 2.6e-116;
tive 0; Mismatches 0;
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, GENERAL INFORMATION:
, APPLICANT: Baker, Kevin
, APPLICANT: Eaton, Dan
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Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
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JS-10-243-282-114
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APPLICANT: Zhang, Zemin
APPLICANT: Shang, Zemin
APPLICANT: Pong, Sherman
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C56
CURRENT APPLICATION NUMBER: U5/10/243,261
CURRENT PILING DATE: 2002-09-13
PRIOR PILING DATE: 2002-09-14
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-11-10
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-06-02
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PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 114
                                                                                                                                                                                                                   Score 1218; DB 12; Length 231;
Pred. No. 2.6e-116;
0; Mismatches 0; Indels 32
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Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
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Goddard, Audrey
Grimaldi, J. Christopher
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Best Local Similarity 87.8%;
Matches 231; Conservative
                                                                                                                                           TYPE: PRT
ORGANISM: Homo Sapien
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US-10-243-261-114
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149 PNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVV 208
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C50
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER: 0F SEQ ID NOS: 116
SEQ ID NO 114
LENGTH: 231
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Best Local Similarity 87.8%; Pred. No. 2.6e-116;
Matches 231; Conservative 0; Mismatches 0;
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CURENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: UJ/197942
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 2002-07-18
PRIOR PLICATION NUMBER: 60/063046
PRIOR APPLICATION NUMBER: 60/063046
PRIOR APPLICATION NUMBER: 60/063046
PRIOR PLING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR PLILNG DATE: 1997-11-10
PRIOR PLILNG DATE: 1998-03-27
PRIOR PLILNG DATE: 1998-03-27
PRIOR PLILNG DATE: 1998-05-22
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Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
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Publication No. US20030138901A1
GENERAL INFORMATION:
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Watanbe, Colin
Wood, William
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APPLICANT: Eaton, Dan
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US-10-243-431-114
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PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR PILING DATE: 1998-06-34
PRIOR PILING DATE: 1998-06-34
PRIOR PLING DATE: 1998-06-35
PRIOR PLING DATE: 1998-06-35
PRIOR PLING DATE: 1998-06-15
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                                                                                                                                                                                                                                                     85.1%; Score 1218; DB 12; Length 231; 87.8%; Pred. No. 2.6e-116; cive 0; Mismatches 0; Indels 32
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PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR PELING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/065027
PRIOR PILING DATE: 1997-11-10
PRIOR PILING DATE: 1998-03-27
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                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 87.8
Matches 231; Conservative
                                                                                                                                                                                                      ; ORGANISM: Homo Sapien
US-10-243-282-114
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                                                                                                                                                         SEQ ID NO 114
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                                                                                                                                                                                          TYPE: PRT
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APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Zhong, Sherman
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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SEQ ID NO 114
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PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR PELING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
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PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-110-24
PRIOR PILING DATE: 1997-110-24
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Filvaroff, Ellen
Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
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Publication No. US20030138903A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CORGANISM: Homo Sapien
US-10-243-402-114
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121 TSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHA 180
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PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR PLEIGNATION NUMBER: 60/086478
PRIOR PLILING DATE: 1998-06-02
PRIOR PLILING DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-03
PRIOR PLING DATE: 1998-06-18
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Search completed: December 12, 2003, 12:24:05 Job time : 49.1424 secs

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1247.959 Million cell updates/sec
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1432
1 MMPKHCFLGFLIGFFLTGVA......YQPMLDRRSQRSEERCVEIP 263
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

CRF2-S1 OR IL22BP. Homo sapiens (Human).

[1] SEQUENCE FROM N.A. NCBI_TaxID=9606;

01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DBC-2003 (TrEMBLrel. 2) Last annotation update)
Soluble cytokine class II receptor, long isoform precursor (Interleukin 22-binding protein CRF2-10L).

263 AA.

PRT;

PRELIMINARY;

096915

RESULT 1 096915 TISSUE-Placenta;
MEDLINE-21518574; PubMed=11607789;
Gruenberg B.H., Schoenemeyer A., Weiss B., Toschi L., Kunz S., Wolk K., Asadullah K., Sabat R.;
"A novel, soluble homologue of the human IL-10 receptor with preferential expression in placenta.";
Genes Immun. 2:329-334(2001). OCH

SUMMARIES		Description	Q96915 homo sapien	096a41 homo	OBOGIN POMO		отом 948960	O8bw64 mus	0968h7 homo sapien		2 O9hb22 homo sapien	Q99ND6 099Nd6 rattus norv		Q90W13 Q90W13 oncorhynchu	Q9YHW0 Q9YHW0 qallus qall	O9PVJ9 qallus qall	0	
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SEQUENCE FROM N.A.

MEDILINE=21286453; Pubmed=11390454;

A REDLINE=21286453; Pubmed=11390454;

A Dickensheers H., Donnelly R.P., Pestka S.;

Identification, cloning, and characterization of a novel soluble receptor that binds 111-22 and neutralizes its activity.";

J. Immunol. 166:7096-7103(2001). Junc.

E RBH; AJ13162; CAC85635.1; -..

R EMBL; A70406671; ARCS715.1; -..

R Genew; HOW00282; Cytok_receptor_2.

R InterPro; IPR000282; Cytok_receptor_2.

R InterPro; IPR000282; Cytok_receptor_2.

T SIGNAL

T SIGNAL

T CHAIN

22 263 SOLUBLE CYTOKINE CLASS II RECEPTOR, LONG

POTENTIAL, SOLUBLE CYTOKINE CLASS II RECEPTOR, LONG ISOFORM.

44 44	Q9ynv9 gallus gall Q9cyk5 mus musculu Q9pvk0 gallus gall Q9by69 homo sapien Q9gk66 ovis aries Q8c352 mus musculu Q63953 mus musculu Q14936 homo sapien Q15467 homo sapien Q9bua0 homo sapien		QSKYM9 trichomonas
4 Q81U57 11 Q8VHM7 12 Q8VZH7 4 Q8VZZZ 11 Q8KZQI	113 Q9XHV9 113 Q9ECKS 113 Q9EVK0 4 Q9EX69 6 Q9GX86 6 Q9GX85 11 Q63953 4 Q14936 4 Q15467 4 O9EUX0	71974 7 0	II VYCKFS 5 Q9XYM9 ALIGNMENTS
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Best Local Similarity 87.8%;
Matches 231; Conservative
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Best Local Similarity 79.6%;
Matches 125; Conservative
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231
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 19, Last sequence update)
Soluble cytokine class II receptor, short isoform precursor (Interleukin 22-binding protein) (RF2-10) (Class II cytokine receptor)
(Interleukin-22 binding protein) CRF2-10) (Class II cytokine receptor)
CRF2-SI OR IL22BP OR IL22RA2 OR IL-22BP.
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MEDLINE=21996522; PubMed=11481447;

Xu W., Presnell S.R., Parrish-Novak J., Kindsvogel W., Jaspers S.,

Chen Z., Dillon S.R., Gao Z., Gilbert T., Madden K., Schlutsmeyer

Yao L., Whitmore T.E., Chandrasekher Y., Grant F.J., Maurer M.,

Cleginek L., Storey H., Brender T., Hammond A., Topouzis S.,

Clegg C.H., Foster D.C.,

"A soluble class II cytokine receptor, IL-22RA2, is a naturally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kotenko S.V., Izotova L.S., Mirochnitchenko O.V., Esterova E., Dickensheets H., Donnelly R.P., Pestka S.; Identification, cloning, and characterization of a novel soluble receptor that binds IL-22 and neutralizes its activity."; J. Immunol. 166:7096-7103 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                     ö
                         Query Match
100.0%; Score 1432; DB 4; Length 263;
Best Local Similarity 100.0%; Prad. No. 1.7e-131;
Matches 263; Conservative 0; Mismatches 0; Indels 0
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TISSUS=Ammnary gland;
MEDLINE=215.18574; PubMed=11607789;
MEDLINE=215.18574; PubMed=11607789;
Gruenberg B.H., Schoenemeyer A., Weiss B., Toschi L., Kunz S. Wolk K., Asadullah K., Sabat R.;
"A novel, soluble homologue of the human IL-10 receptor with perferential expression in placenta.";
Genes Immun. 2:329-334(2001).
 C96ECEC5D78AC79B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           occurring IL-22 antagonist.";
Proc. Natl. Acad. Sci. U.S.A. 98:9511-9516(2001).
                                                                                                                                                                                                                                                                                                                                                                                                               231 AA
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                                                                                                                                                                                                                                                                                                             AEIYOPMLDRRSQRSEERCVEIP 263
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30550 MW;
                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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 263 AA;
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SEQUENCE
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                                                                                                                                                                                                                                                                              SOLUBLE CYTOKINE CLASS II RECEPTOR, SHORT ISOFORM.
24A6912BFF75100F CRC64;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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"Cloning and characterization of Interelukin-22 Binding Protein 22BP), a natural antagonist of Interelukin-22."; submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AJ313161; CAC85634.1; ... EMBL, AV404566; AAK85714.1; ... EMBL, AX040566; AAK87714.1; ... EMBL, AY04228; CAC83097.1; ... EMBL; AY064229; CAC83097.1; ... Interpro; IPR000282; Cytok_receptor_2.
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EMBL, AV046568; AAK85716.1; InterPro; IPR000282; Cytok receptor 2.

ERGUINGE 130 AA; 15128 WW; A165814C641F5E5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               Length 231;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Interleukin 22-binding protein CRF2-108.
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Pred. No. 1.1e-110;
0; Mismatches 0;
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Pred. No. 2e-57;
0; Mismatches 0
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RESULT 4
10 904HF4
10 904HF4
10 904HH
AC 094HH
DT 01-M

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76 -----YGQKKWINKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 126
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STRAIN=C57BL/6J; TISSUE=Oviduct;

MEDLINE=22154683; PubMed=12466851;

The FANTOM CONSOrtium,

The FANTOM Consortium,

"Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";

Nature 420:563-573(2002).

SEMBL, AKO54215; BAC33695.1;

SEQUENCE 546 AA; 61978 MW; E7EC07DA2D49AF7F CRC64;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
    Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                    Length 553;
                                                                                                                                                                                                                                                                                               Query Match
21.6%; Score 310; DB 4; Length 55:
Best Local Similarity 32.0%; Pred. No. 1.3e-21;
Matches 74; Conservative 33; Mismatches 90; Indels
                                                                               SEQUENCE FROM N.A.
Griffiths C.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, Al135902, CAC38375.1;
InterPro; IFR00282; Cytok receptor_2.
InterPro; IPR01187; Tissue_factor.
Pfam; PF01108; Tissue_factor.
                                                                                                                                                                                                                                                          553 AA; 62485 MW; D5C2621FDC848328 CRC64;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                        Mammalia; Eutheria;
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      Sukaryota; Metazoa;
                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                      Receptor.
SEQUENCE
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Best Local 8
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FVQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDL 120
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                                          ---YGORÓWKNKEDCWGTÓELSCDL 88
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Lok S., Kho C., Jelmberg A., Adams R., Whitmore T., Farrah T., O'Hara P., Hara P., Homo sapiens cytokine receptor homolog.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
(Interleukin 20 receptor alpha, isoform 1).
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                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-GCT-2002 (TrEMBLrel. 22, Last annotation update)
Class II cytokine receptor ZCYTOR?.
                                                                                                        121 TSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWE
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InterPro; IPR001281; Cytok receptor 2.
InterPro; IPR001187; Tissue factor.
Pfam; PF01108; Tissue_fac; I.
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                                       61 FVQYKI-----
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SEQUENCE FROM N.A.
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01-DEC-2001 (
01-MAR-2003 (
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SEQUENCE
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096SHB **096SH8**

096SH8 ID 09 AC 09 DT 01 DT 01 DE BA GN 11L

RESULT 5

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69; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    $ 252
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Query Match
Best Local S
Matches 69
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SEQUENCE
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  130 ERFYPFLETQVSPPEVALTTGEKSISIALTAPEKWKRNPQDHTVSMQQIYPNLKYNVSVY 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 208
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                                         NNSLEKEQKVYEG--AHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCV 260
                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.3%; Score 262; DB 4; Length 209; 31.1%; Pred. No. 1.8e-17; ive 29; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butel
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 KPANITPLSINMKUVLQWTPPEGLQGVKVTYTVQYFI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Griffiths C.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL135902; CAC38376.1; -.
InterPro; IPR000282; Cytok_receptor_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.; Strausberg R.; Strausberg R.; Strausberg R.; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC020213; AAH29273.1; Genew; HGNC.13700; IL22RA1. InterPro; IPR000282; Cytok_receptor_2.
                                                                                                                                                                                                                                                (TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
(Interleukin 20 receptor alpha, isoform 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               574 AA; 63076 MW; D46CC71D496F3420 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 AA; 23616 MW; 467AB77BE3840361 CRC64;
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Last annotation update)
                                                                                                                                                                                     209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 NTKSNRTVSLKWNGAY 202
                                                                                                                                                                                                                          (TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 22, (TrEMBLrel. 22, (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61; Conservative
                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
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01-MAR-2002
BA204P2.1.3
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01-MAR-2003
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Q96SH7;
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Q8N6P7;
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10 696 SH7
10 096 SH7
10 01-D
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10 01-D
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                                                                                                                                                                                                               77 OKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVR 136
                                                                                                                                                                                                                                                                                                                         137 AASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIE 196
                                                                                                                                                                                                                                                                                                                                                               98 AVSAGGRSATKWIDRFSSLQHTILKPPDVICISKVRSIQMIVHPTPTPIRAGDGHRLILE 157
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                                                                                                                                                                                                                                                 21 GTQSTHESLKP----QRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE=20469498; PubMed=10875937;
Axie M.H., Aggarwal S., Ho W.H., Foster J., Zhang Z., Stinson J.,
Axie M.H., Aggarwal S., Gurney A.L.;
Wood W.I., Goddard A.D., Gurney A.L.;
"Interleukin (IL)-22, a Novel Human Cytokine That Signals through the
Interferon Receptor-related Proteins CRF2-4 and IL-22R.";
J. Biol. Chem. 275:31335-3139(2000).

EMBL; AF286095; AAG22073.1; -.
                                                                                                                                    197 D-YYELLYRVFIINNSLEKEQKVYE----GAHRAVEIEALTPHSSYCVVAEIYQPMLDRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTOSTHESLKP----ORVOFOSRNFHNILOWOPGRALIGNSSVYFVOYKIMFSCSMKSSH
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     Length 574;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutel
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
16.8%; Score 240; DB 4; Lv 28.6%; Pred. No. 8.9e-15; ive 31; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.8%; Score 240; DB 4;
llarity 28.6%; Pred. No. 8.9e-15;
Conservative 31; Mismatches 93
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2003 (TrEMBLrel. 23,
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90 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 L----------NVTECDVSS--LSVYGAYVLRVRTEWEDEHSDWAVV 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 KPRNARISSVNFRSVLLMDPPGVRKGNLS-YTVQAKSIF------PKQNFNNVTTN 71
                                                                                                                                                                                                                                                                                                                                                                                                                              30 KPORVOFOSRNFHNILOWOPGRALIGNSSVYFVOYKIMFSCSMKSSHOKPSGCWOHISCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 259
  D., Uze G., Lutfalla G.;
the interferon/interleukin-10
                                                                                                                                                                                                                                                                                                                                       1 12.6%; Score 180.5; DB 13; Length 341; Similarity 24.2%; Pred. No. 3e-09; 56; Conservative 37; Mismatches 97; Indels 41;
                                                                                                                                                                                                                                                                                        341 AA; 39062 MW; 18027239BF8A9C87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294
                                                       PRT;
Reboul J., Gardiner K., Monneron Comparative genomic analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 294 T.
294 AA; 33404 MW;
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                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 24.2*
Matches 56; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue factor precursor.
                                            receptor gene cluster.
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tes 74; Conserv
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 VYFVQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGSLLVILHAPNLPYRYQKEKNVSIEDYYE-----LLYRVFI-----INNSLEKEQ 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLPR--LLPFLVSISSLSLGFRAHGTELPSPSSVWFBARFFQHILRWMSIPNO----SES
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                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Archosauria, Aves; Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

TISSUE-Peripheral blood;
Ward H., Vigues S., Poole S., Bristow A.F.;
"The rat interleukin-10 receptor: cloning and sequencing of cDNA coding for the alpha-chain protein sequence, and demonstration by western blotting of expression in rathrain.";
Cytokine 0:0-0(0).

EMBL, AJ305049; CAC24567.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.4%; Score 192.5; DB 11; Length 569; 25.2%; Pred. No. 3.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 KVYEGAHRAVEIEALTPHSSYCVVAEIYOPMLDRRSQRSEERCVEI 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 FTLEVPKRM------RKFCVKVMPHVESRINKAEWSEEQCLHV 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 16 POTENTIAL.
17 569 INTERLEUKIN-10 RECEPTOR.
569 AA, 63526 MW, 2354FD61DB351BD2 CRC64;
                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                          Interleukin-10 receptor, alpha chain precursor
                                                                                                                      569 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interleukin-10 receptor 2.
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                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
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             $ 212
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01-MAR-2003
             212
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Sangrador-Vegas A., Smith T.J.;
Sangrador-Vegas A., Smith T.J.;
Sangrador-Vegas A., Smith T.J.;
Sangrador-Vegas A., Smith T.J.;
"Molecular cloning of rainbow trout (Oncorhynchus mykiss) tissue factor precursor by use of suppression subtractive hybridisation.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ291167, CAC8787.1;
InterPro; IPR000282; Cytok_receptor_2.
InterPro; IPR000187; Tissue_factor.
Pfam; PF01108; Tissue_factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 GFLIS--FFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei; Euteleostei;
Protacanthopterygii, Salmoniformes; Salmonidae, Oncorhynchus.
163 KKGSNKKVIHIDIKHNSEILSQLEPWTIYCIQVQGVIPEWNKTGERSQELC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.1%; Score 173.5; DB 13; Length 26.8%; Pred. No. 1.2e-08; tive 34; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
TISSUE FACTOR.
105DDDA107E54EDE CRC64;
                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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NON TER
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Matches
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           RESULT 14
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                                                                                                                                  224 PIHC-----IKTTRKVNDLLCPTNVRVFALNMKFYLLWDNHY----NEHVTYT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 VQYLTGY---LKNLYDDYSSKWQKVS----GCENIT------SMKCNLS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVIKPTSASYYPRVQAMA--EYSKSCLSK-----DVEVDPPVTNEIGPPDVKVDISD-- 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 GSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSL--EKEQKVYEGAHRAVEIE 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSD 126
                                                                                        174 LLVILHAPN-LPYRYQKEKNVSIEDYY--ELLYRVFIIN--NSLEKEQKVYEGAHRAVEI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMN------ITQVN 171
                                                                          IQEPYYGRVRAASAGSYSE-------WSMTPRFTPWWETKIDPPVMNITQVNGS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
GVLLSSVLFTIGAAGEDYFPEAMD---VQWVSNNFKTILTWGP-----EPTNY--TYTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT
                                                     ------HCIRSSRTECDLINELRN
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13; Length 569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.9%; Score 155.5; DB 13; Length 23.2%; Pred. No. 1.5e-06; ive 38; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6A757DDFB891E605 CRC64;
                                                                                                                                                                                                                                                                 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                              201 TNLDKGQSYCVIVAAYIP--SRSAQKRLGDWSKAQC 234
                                                                                                                                                                 229 EALTPHSSYCVVAEIYQPMLDRRSQR----SEERC 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor gene_cluster.";
Genome Res. 9:242-250(1999).
EMBL; AF082664; AAD13669.1; -.
INTERFOR IPRO00282; Cytok receptor_2.
INTERFO; IPRO03961; FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99177346; PubMed=10077530;
                                                                                                                                                                                                                                                                                                     Interferon alpha/beta receptor 1.
                                                     60 EFSRVCKDRORNP------
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Best Local Similarity 23.2%
                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=Liver;
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121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 GSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSL--EKEOKVYEGAHRAVEIE 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 VOYKIMPSCSMKSSHOKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 PKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSV-YF
                                                                                                                                                                                        Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99177346; PubMed=10077530; Reboul J., Gardiner K., Monneron D., Uze G., Lutfalla G.; "Comparative genomic analysis of the Interferon/Interleukin-10 ereceptor gene cluster."; Genome Res. 9:242-250(1999). EMBL; AF082667; AAD13679.1; -.
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Dumoutler L., Renauld J.C.;
"Cloning and characterization of LICR-2, a new type 2 cytokine receptor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.6%; Score 152.5; DB 13; Length 442; 22.9%; Pred. No. 2.2e-06; tive 39; Mismatches 101; Indels 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Soluble isoform of Likely interleukin or cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butel.
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442 AA; 49877 MW; 839EBE92170609E0 CRC64;
                                                                           01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Interferon alpha/beta receptor 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 ALTPHSSYCVVAEIYQPMLDRRSQRSEERCV 260
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  442 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000282; Cytok receptor_2.
InterPro; IPR003961; FN_III.
                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
hes 62; Conserv
                                                                                                                                                                                                                                                                                                                                [1] SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor.
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Query Match 10.5%; Score 151; DB 4; Length 244;
Best Local Similarity 24.3%; Pred. No. 1.5e-06;
Matches 63; Conservative 32; Mismatches 76; Indels 88; Gaps 13;
                                                                                                                                                                                                                                         89 NFPGCRILAKYGORQWKNKEDCWGTQELSCDLTS-ETSDIQEPYYGRVRAASAGSYSEWS 147
                                                                                                                                                                                                                                                                                                                      148 MTPRFTPWWETKIDPPVMNITQVNGSLLVILHA-----PNLPYRYQKEKNVSIEDYYE 200
                                                                                                                                                                                                                                                                                                                                               65 ------RRWREVEECAGTKELLCSWMCLKKQDLYNKFKGRVRTVSPSSKSPWV 112
                                                                                                                                                                                                                                                                                                                                                                                                      201 LLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSS------YCVVAE-IYQP 246
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                                                                                                                                                            31 PORVOPOSRNFHNILOWOPGRALIGNSS--VYFVOYKIMFSCSMKSSHOKPSGCWQHISC 88
                                                                                                                                                                                   27 PONUTLLSQNFSUYLTWING---LGNPQDVTYFVAYQ-----SSPT-----64
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AJ534331; CAD58830.1; -- SEQUENCE 244 AA; 27536 MW; A6F3310C13FCC083 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 MLDRRSQRSEERC--VEIP 263
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Search completed: December 12, 2003, 12:27:20 Job time : 56.383 secs

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December 12, 2003, 12:15:52 ; Search time 66.8644 Seconds (without alignments) 624.325 Million cell updates/sec
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| SIDSI/gcgdata/geneseqfgeneseqp-embl/AA1994.DAT:+
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| SIDSI/gcgdata/geneseqfgeneseqp-embl/AA1997.DAT:+
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| SIDS1/gcgdata/geneseqgeneseqp-emb1/AA1985.DAT:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Cytokine receptor Human cytokine rec Human IL-TIF/IL-22 Human Pro peptide Human cytokine rec Human cytokine rec Human cytokine rec Cytokine receptor Cytokine receptor Cytokine receptor Cytokine receptor Cytokine receptor	recept recept recept recept recept recept recept cokine	Human Zcytor16 ext Human DAMX cytokin Human Cytokine rec Cytokine receptor Mouse Zcytor16 pro Mouse Zcytor16 pro Cytokine receptor Human IL-20 recept Interleukin-20 sub Human IL-20 recept Interleukin-20 sub IL-20R-16 gammal IL-20R-16 gammal Interleukin-20 sub IL-20R-16 gammal Interleukin-20 sub Human IL-20 recept Interleukin-20 sub Human IL-20 recept Interleukin-20 sub Human IL-20R-16 gammal
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231 231 231 231 231 231 231	2331 2331 2331 220 20 20 20 20 20 20 20 20 20 20 20 20	210 249 249 230 230 230 130 130 201 214 2114 2114 2117
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ALIGNMENTS

ABJ10499 standard; Protein; 263 AA

RESULT 1 ABJ10499

antiinflämmatory; interleukin-antagonist-20; interleukin-antagonist-22; gene therapy; interferon-antagonist-alpha; interferon-antagonist-beta; interferon-antagonist-gamma; cytokine receptor family 2; CFF2-12; autoimmune disease; rheumatoid arthritis; multiple sclerosis; Immunosuppressive; antirheumatic; antiarthritic; neuroprotective; Cytokine receptor family 2 (CRF2) related protein SEQ ID No 4. 12-JAN-2001; 2001US-261442P. 06-FEB-2001; 2001US-267021P. 23-FEB-2001; 2001US-270835P. 14-JAN-2002; 2002WO-US00986 (first entry) (GEMY) GENETICS INST LLC. WO200266647-A2 inflammation. Unidentified 21-NOV-2002 29-AUG-2002 ABJ10499;

Deng B;

Fouser L, Liu W,

Lai Y, Martensen SA; ang Z, Xie Q, Rizni SK;

Kabnic KS, Lai Y, Strum JC, Xiang Z,

Cogswell JP, Smith RF,

Agarwal P, Murdock PR, 2002-139783/18.

N-PSDB; AAD27816

BEECHAM CORP. BEECHAM PLC.

) SMITHKLINE BEECH) SMITHKLINE BEECH) GLAXO GROUP LTD.

(SMIK) (SMIK) (SMIK) (GLAX)

22.-UUN-2001; 2001WO-US19929. 22-UUN-2000; 2000US-213156P. 22-JUN-2000; 2000US-213161P.

WO200198342-A1.

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                                                                                                                                                        (CRF2-12) nucleic acid molecule encoding a polypeptide with amino acids 21-66 of a 231 residue amino acid sequence, given in the specification, or its complement. The compositions and methods of the present invention are useful for disgnosing, screening and treating disorders associated with abnormal CRF2-12 activity such as autoimmune diseases like rheumatoid arthritis, multiple sclerosis and inflammation. This sequence represents a cytokine receptor family 2 (CRF2-12) protein relating to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; therapy; wound healing disorder; vaccine; cancer; infection; autoimmune disorder; haematopoietic disorder; inflammation; arthritis; parkineno; disorder; haematopoietic disorder; inflammation; arthritis; parkineno; disorder; halpaimer; schores; halpaimer; disorder; analgesic; cardiant; asthma; ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder; depression; cardiovascullar disease; myocardial infarction; renal failure; respiratory disease; liver disorder; Fanconi's sydenome; spleen disorder; type II diabetes mellitus; skeletal muscle disorder; immunosuppressive; hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease; nootropic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory; haemostatic; vulnerary; anticonvulsant; antirheumatic; neuroprotective; nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;
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                                                New isolated CRF2-12 nucleic acid encoding a polypeptide, useful for diagnosing and treating disorders with abnormal CRF2-12 activity such as autoimmune diseases like rheumatoid arthritis, multiple sclerosis and inflammation -
                                                                                                                                                                                                                                                                                                                                                                                 FVQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDL
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                                                                                                                                              The invention relates to an isolated type 2 cytokine receptor family
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                                                                                                                   Claim 2; Page 7; 91pp; English.
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                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
1es 263; Conservative
            2002-674946/72
                                                                                                                                                                                                                                                                                  263 AA;
                         N-PSDB; ABT08217
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The invention relates to secreted and membrane-associated polypeptides and polynucleotides. The sequences of the invention are useful in diagnostic assays for detecting diseases associated with inappropriate cativity or levels of these polynucleotides, and in identifying their agonists and antagonists that are potentially useful in therapy. The sequences of the invention are useful as vaccines for inducing immunological response. The sequences of the invention are useful for treating cancers, infections, autoimmune disorders, haematopoletic disorders, wound healing disorders, cholesteryl ester storage disease, infections alsorders, infections alsorders, cholesteryl ester storage disease, infections, alloss, consential muscular dystrophy, junctional epidermolysis bullosa, Parkinson's disease, Hurhington's chorea, multiple sclerosis, viral and bacterial infections, Alzheimer's disease, asthma, arthritis, allergies, schizophremia, sp8442445pRoa-associated disorders, septicaemia, psoriasis, inflammatory bowel disease, transplant rejection, graft verse host disease, ischaemia, stroke, acute respiratory disease, syndrome, restenosis, brain injury, AIDS, bone diseases, action, depression, anxiety disorders and myconic dystrophy, depression, anxiety disorders and sleep disorders, cation, anxiety disorders and myconic dystrophy, diseases including congestive heart failure and myconic dystroph, diseases including congestive heart failure and myconic dystrophy.
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Novel secreted and membrane-associated polypeptides and polynucleotides useful for preventing, ameliorating or correcting dysfunction or disease including diabetes, cancer, hypertension and growth
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Pred. No. 6.7e-135;
; Mismatches 0;
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                                                                                                                                                                                                                                   Claim 1; Page 133-134; 138pp; English.
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inflammatory disorder; infectious disorder; immunodeficiency disorder; autoimmune disorder; renal disease; demyelinating disease; skin disease; neoplasia; transplantation associated disease; immunosuppressive; anti-inflammatory; antiasthmatic; antidiabetic.
                                                                                             Gurney AL;
FVQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDL
                      TSETSDIOEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHA
                                                                                                                                                     PNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRO19598; clone DNA145887; immune-related disorder;
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/label= Mature_PRO19598_polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "N-myristoylation site"
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/label= Signal_peptide
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                                                                                                                                                                                                                                AEIYQPMLDRRSQRSEERCVEIP
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2000US-209832P.
2000WO-US23328.
2000WO-US32678.
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2000US-191015P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human PRO19598 polypeptide.
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides the protein and coding sequences of 3 variants of a human cytokine receptor. The sequences can be used in the diagnosis, prevention and treatment of immune diseases, including psoriasis, cancer, chronic/life-threatening infections, rheumatoid arthritis, multiple sclerosis, Crohn's disease, ulcerative colitis and transplant rejection and in reproductive medicine, e.g. for diagnosing abnormal immune reactions which cause abortions. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY
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                                                          PNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding soluble cytokine receptor, useful for diagnosis and treatment of e.g. immune disease, also related protein
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Pred. No. 1.7e-134;
1; Mismatches 0;
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                                                                                                                                     AEIYQPMLDRRSQRSEERCVEIP 263
                                                                                                                                                                                                                                                                         Ź
                                                                                                                                                                                                                                                                                                                                                                                            Human cytokine receptor variant 3.
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                                                                                                                                                                                                                                                                         AAO17382 standard; Protein; 263
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17-NOV-2000; 2000DB-1058907.
19-DEC-2000; 2000DE-1064906.
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Best Local Similarity 99.6
Matches 262; Conservative
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The present invention relates to the isolation of 9 novel human PRO polypeptides and the CDNA sequences (AAS15360-AAS15368) encoding them. The novel PRO polypeptides include PRO1356, PRO1368, PRO13684, PRO3144, PRO3151, PRO91822, PRO9964, PRO1008 and PRO19598. The CDNA sequences encoding these PRO polypeptides have been designated as clones. DNA648081-1553, DNA84188-2520, DNA87997, DNA89273, DNA864866-1601, DNA64903-1553, DNA8418-2520, DNA87997, DNA89273, DNA95223-2567, DNA969973, DNA8101921 and DNA145887 respectively.

COMPOSITIONS (e.g. vaccines) containing PRO polypeptides and methods of inflammatory disorders. Such disorders include immune-mediated inflammatory disorders (e.g. osteoarthritis), non-immune-mediated inflammatory disorders (e.g. osteoarthritis), non-immune-mediated inflammatory disorders (e.g. osteoarthritis), infectious disorder
                                                                                                                                                                                               Nucleic acids encoding PRO polypeptides, useful for detecting and treating immune related diseases and disorders in mammals including autoimmune diseases, inflammatory diseases and asthma -
                             Zhang Z;
                             Wood WI,
                                                                                                                                                                                                                                                                                                                                         Claim 10; Fig 18; 122pp; English.
                          Watanabe CK,
                                                                                      2001-625876/72.
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                                                                                                                                   N-PSDB; AAS15368
                             Tumas D,
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                                                                  2 MPKHCFLGFFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF
                                                                                       1 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQFGRALTGNSSVYF
                                                                                                                                                          61 VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT
                                                                                                                                                                                                      SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP
                                      Gaps
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99.7%; Score 1427; DB 22; Length 262; 100.0%; Pred. No. 2.18-134; ive 0; Mismatches 0; Indels 0
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                 Best Local Similarity 100.
Matches 262, Conservative
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Human; soluble protein; interleukin-TIF/IL-22; IL-TIF/IL-22; IL-22BP;
IL-TIF/IL-22 antagonist.
                                                                                     Human IL-TIF/IL-22 binding protein #2.
                    AAU80324 standard; Protein; 263 AA
                                                                (first entry)
                                                                15-JUL-2002
                                           AAU80324;
RESULT 5
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The present invention relates to a new polymucleotide that encodes a soluble protein which binds to interleukin (IL)-TIF/IL-22 (also referred to as IL-22B), where the complementary sequence of the invention by the tringent conditions to a nucleotide sequence of 271 or 2366 base pairs, as given in the specification. The molecules of the invention are useful for inhibiting (antagoniaing) effect of IL-TIF/IL-22 on a cell, for determining whether IL-TIF/IL-22 is present in a sample, for inhibiting binding of IL-TIF/IL-22 to a binding partner, preferably in vitro, and for obtaining an antibody molecule specific for the soluble binding sprotein of the invention, from a population or panel of antibody molecules of diverse binding specificity. The soluble protein is further useful in manufacture of a medicament for treating an IL-22 mediated fasease and for assaying an asent, preferably an antibody or a peptide fragment of IL-TIF/IL-22 or the soluble protein, that modulates binding of the soluble protein to IL-TIF/IL-22, where the agent identified is used in the manufacture of medicament for treating IL-TIF/IL-22 mediated discorder. The antibody is useful for determining presence of the soluble protein, where the antibody is detectably labelled. The present amino acid sequence represents the human IL-TIF/IL-22 binding protein #2 of
                                                                                                                                                                                                                                                                                                                                                                                        Polynuclectide and polypeptide of soluble protein which binds to interleukin-TIF/IL-22 useful for inhibiting effect of IL-TIF/IL-22 on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 14; Page 41-42; 42pp; English
                                                                                                                                                                                                                                    (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                            22-SEP-2000; 2000US-234583P.
03-NOV-2000; 2000US-245495P.
31-JUL-2001; 2001US-0919162.
                                                                                                      21-SEP-2001; 2001WO-US29576.
                                                                                                                                                                                                                                                                                Dumoutier L;
                                                                                                                                                                                                                                                                                                                      WPI; 2002-383190/41.
N-PSDB; ABK50080.
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                    WO200224912-A2
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                                                             28-MAR-2002
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120 240 120 180 121 TSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHA 180 240 9 9 PNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVV 61 FVQYKIMFSCSMKSSHQSQVDAWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDL PNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVV 1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY 1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY PVQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDL TSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHA Gaps ô Score 1397; DB 23; Length 263; Pred. No. 2.1e-131; 0; Mismatches 5; Indels 0; 241 AEIYQPMLDRRSQRSEERCVEIP 97.6%; Query Match Best Local Similarity 98.1 Matches 258; Conservative 61 121 181 181 용 ઠે 원 ò 용 ò 용 ò ઠે

Homo sapiens

AEIYQPMLDRRSQRSEERCVEIP

241

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RESULT

(first entry)

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Human DNAX cytokine receptor subunit 4.2 (DCRS4.2).
      AAE02460 standard; Protein; 231 AA.
                                             10-AUG-2001
                          AAE02460;
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                                                                                                                                                                                                                                                                                                                                           The patent discloses novel human cytokine, ZCYTO18 protein and its corresponding DNA. ZCYTO18 protein induces proliferation of cells expressing zcytoril, a receptor for ZCYTO18 or induces cytotoxicity in K5626 cells. ZCYTO18 DNA is useful for detecting a genetic abnormality in a patient. ZCYTO18 DNA and its antibodies are useful for detecting cancer and inflammation. ZCYTO18 protein is useful for killing cancer cells. It is useful for increasing platelets in a patient or injured tissue. It is also used in gene therapy. The present sequence is human zcytor16, which is a naturally expressed soluble receptor antagonist of ZCYTO18 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human cytokine polypeptide, ZCYT018, useful for treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MMPKHCFLGFLISFFLIGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY
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                                                                                    Human, cytostatic, cytokine, ZCYTO18 protein, genetic abnormality,
cancer, inflammation, gene therapy, zcytor16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 231;
                                                                  Human ZCYTO18 soluble receptor antagonist, zcytor16 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1218; DB 22;
Pred. No. 1.5e-113;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                          Example 13A; Page 158-159; 167pp; English.
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       AAE05048 standard; Protein; 231 AA
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01-DEC-2000; 2000US-0250841.
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                                               (first entry)
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                                                                                                                                                                                                                                                     Kindsvogel
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                                                                                                                    Homo sapiens
                                               10-SEP-2001
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                           AAE05048;
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The present sequence is human DNAX cytokine receptor subunit 4.2

(DCRS4.2). DCRS4 gene is located on chromosome 6q24.1-25.2.

(Cytokine receptors, fragments and antibodies are useful for treating immunological disorders. DCRS3 (50R), DCRS4 (cytor) or fragments are useful in drug screening to identify compounds having binding affinity the receptor subunit. Modulators of DCRS are useful for modulating the physiology or development of a cell or tissue culture cells. A purified DCRS is useful as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to production of antibody to the endogenous receptor. Cytokine receptor sequences are useful as probes for detecting levels of the cytokine receptor in patients suspected of having an immunological disorder. Antibodies have therapeutic value, are useful as potent antagonist, in detecting or quantifying ligands, for isolating DCRS proteins and peptides, to screen expression libraries for particular expression products, to raise anti-idiotypic antibodies and for detecting or diagnosing various immunological conditions related to expression of the protein or cells which express the protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New mammalian receptor proteins related to cytokine receptors, useful for regulating cell development and for diagnosis and treatment of immunological disorders
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Human; immunomodulator; DNAX cytokine receptor subunit 4.2; DCR84.2;
therapy; immunological disorder; drug screening; cell development;
chromosome 6q24.1-25.2.
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/labbl= DCRS4.2
/note= "Human mature DNAX cytokine receptor
subunit 4.2"
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Pred. No. 1.5e-113;
0; Mismatches 0;
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/label= Signal-peptide
22..231
                                                                                                                                                                                                                Location/Qualifiers
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Best Local Similarity 87.8%;
Matches 231; Conservative (
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N-PSDB; AAD06414.
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RESULT 7

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231 AA;
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Matches 231;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a human cytokine receptor polypeptide, designated zcytor16. The zcytor16 polypeptide can be expressed by standard recombinant methodology and can bind to IL-TIF (undefined). The zcytor16 protein is useful for: inhibiting IL-TIF induced proliferation or differentiation of hematopoietic cell(s) (progenitors); reducing IL-TIF induced or IL-9 induced inflammation, and suppressing an inflammation receptor polypeptides such as soluble zcytor 16/CRF2-4 can be used to reduce progression and symptoms of cancer. Zcytor16 polypeptides
                         88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         soluble cytokine receptor polypeptides and polynucleotides, useful diagnosing and treating cancer and inflammatory conditions -
                                                      TSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHA
                                                                                            PNLPYRYQKEKAVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVV
                         -----YGQRQWKNKEDCWGTQELSCDL
                                            TSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHA
        FVQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDL
                                                                                                                                                                                                                                                                   Cytokine receptor; zcytor16; IL-TIF; antiinflammatory; cytostatic; antirheumatic; antiarthritic; antiasthmatic; antiatherosclerotic; immunosuppressive; chromosome 6q24.1-25.2; human.
                                                                                                                                                                                                                                                                                                                                                                   domain"
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'--re= "extracellular
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                                                                                                                                       AEIYOPMLDRRSORSEERCVEIP 231
                                                                                                                                                                                                                                                                                                                                               "Ig domain 1"
                                                                                                                                                                                                                                                                                                                                                                                       /note= "Ig domain 2"
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                                                                                                                                                                                                                                                  Human cytokine receptor, zcytor16.
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13-SEP-2000; 2000US-0232219.
31-OCT-2000; 2000US-0244610.
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                                                                                                                                                                                                                              (first entry)
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112..210
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/note= "
                           FVQYKI----
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can also be used to detect IL-TIF levels which is indicative of pathological conditions including inflammatory states (e.g. rheumatoid arthritis) and cancer. Antibodies that bind zcytoris polypeptides and topolypeptides themselves are useful for the treatment of inflammation, inflammatory diseases (e.g. infection, asthma, inflammatory bowel disease, rheumatoid arthritis and atherosclerosis) and autoimmune diseases. The antibodies and acytoris polymucleotides are also useful for detecting cancer. The present sequence represents the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHA
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                                                                                                                                                                                                                                                                                                                                                              Length 231;
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220..223
                                                                                                                                                                                                                                                                                                                                                          Similarity 87.8%; Pred. No. 1.5e-113; 11; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Class II cytokine domain"
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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Zcytor16 protein.
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Immunosuppressive, antirheumatic, antiarthritic, neuroprotective; antinflammatory; interleukin-antagonist-22; gene therapy; interferon-antagonist-alpha; interferon-antagonist-beta; interferon-antagonist-beta; interferon-antagonist-gamma; cytokine receptor family 2; CRF2-12; autoimmune disease; rheumatoid arthritis; multiple sclerosis;

Cytokine receptor family 2 (CRF2) related protein SEQ ID No

(first entry)

21-NOV-2002

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The invention relates to cytokine receptor designated as mouse Zcytor16 which can bind and antagonise the IL-TIF. The Zcytor16 polypeptide is useful in modulating the immune system by binding Zcytor16 ligand, and thus, preventing the himding of the ligand with endogenous Zcytor16 receptor. It is useful for studying human inflammation or immune function, or for treating autoimmune or inflammatory diseases such as function, or for treating autoimmune or inflammatory diseases such as inflammatory bowel disease, rheumatoid arthritis, asthma, systemic upus erythematosus, wyssthenia gravis or allergy, atherosclerosis, cancer, diabetes, glomerulonephritis or pancreatitis, or in assessing therapeutic aspects of IL-TIF, chemical therapeutics, anti-IL-TIF antibodies or Zcytor16 soluble receptors. Zcytor16 DNA and the anti-mouse Zcytor16 antibody are useful as probes in detecting gene expression and gene structure, such as in the indetecting gene expression and gene structure, such as in the placental health and function. It is also used in gene therapy. The present sequence is human Zcytor16 protein. Human Zcytor16 gene resides
                                                                                                                                                                                                                                                                                                                   New Zcytor16 polypeptide useful for treating autoimmune or inflammatory diseases, e.g. inflammatory bowel disease, rheumatoid arthritis, asthma, atherosclerosis, cancer or diabetes, or in assessing
                                                                                                                                                                                                          Chen Z;
                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 191; 221pp; English
                                                                                                                                                                                                          Kindsvogel W,
                                                                                                                                                                                                                                                                                                                                                                                      therapeutic aspects of IL-TIF
                                                                                                    2001US-273035P.
2001US-279232P.
                                                            04-MAR-2002; 2002WO-US06267
                                                                                                                                                                (ZYMO ) ZYMOGENETICS
                                                                                                                                                                                                          Presnell SR, Xu W,
                                                                                                                                                                                                                                                     WPI; 2002-698750/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 AA;
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                                                                                                    02-MAR-2001;
27-MAR-2001;
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12-JAN-2001; 2001US-261442P. 06-FEB-2001; 2001US-267021P. 23-FEB-2001; 2001US-270835P.

Deng B;

WPI; 2002-674946/72. Fouser L, Liu W,

N-PSDB; ABT08216

(GEMY) GENETICS INST LLC.

14-JAN-2002; 2002WO-US00986.

WO200266647-A2 Unidentified inflammation

New isolated CRF2-12 nucleic acid encoding a polypeptide, useful for diagnosing and treating disorders with abnormal CRF2-12 activity such as autoimmune diseases like rheumatoid arthritis, multiple sclerosis

Claim 2; Page 6; 91pp; English

and inflammation

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The invention relates to an isolated type 2 cytokine receptor family (CRED-12) nucleic acid molecule encoding a polypeptide with amino acids 21-66 of a 231 residue amino acid sequence, given in the specification, or its complement. The compositions and methods of the present invention are useful for diagnosing, screening and treating disorders associated with abnormal CRED-12 activity such as autoimmune diseases like rheumatoid archritis, multiple sclerosis and inflammation. This sequence represents a cytokine receptor family 2 (CRF2-12) protein relating to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 TSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVWNITQVNGSLLVILHA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 FVQYKI-----YGQRQWKNKEDCWGTQELSCDL
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Pred. No. 1.5e-113;
0; Mismatches 0;
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Best Local Similarity 87.8%;
Matches 231; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FVQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNLPYRYOKEKNVS1EDYYELLYRVF11NNSLEKEOKVYEGAHRAVE1EALTPHSSYCVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.1%; Score 1218; DB 23; Length 231; 87.8%; Pred. No. 1.5e-113; tive 0; Mismatches 0; Indels 32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEIYOPMLDRRSQRSEERCVEIP 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABJ10498 standard; Protein; 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 97.8
Matches 231; Conservative
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149 241

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ABJ10498

RESULT 10
ABJ10498
ID ABJ1
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231

209 AEIYQPMLDRRSQRSEERCVEIP

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32; Gaps

Indels

Length 231;

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The present invention provides the protein and coding sequences of 3 variants of a human cytokine receptor. The sequences can be used in the diagnosis, prevention and treatment of immune diseases, including psoriasis, cancer, chronic/life-threatening infections, rheumatoid arthitis, multiple solerosis, Crohn's disease, ulcerative colitis and transplant rejection and in reproductive medicine, e.g. for diagnosing abnormal immune reactions which cause abortions. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding soluble cytokine receptor, useful for diagnosis and treatment of e.g. immune disease, also related protein
                                                                                                                                                                       rheumatoid arthritis; multiple sclerosis; Crohn's disease; locarius collitis; transplant rejection; abortion; antipsoriatic; immunosuppressive; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiulcer; cytostatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 23; Length 231;
                                                                                                                                                          Human; cytokine receptor; immune disease; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1218; DB 23;
Pred. No. 1.5e-113;
0; Mismatches 0;
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                               AA017381 standard; Protein; 231 AA
                                                                                                                           Human cytokine receptor variant 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weiss B, Sabat R, Assadullah K,
                                                                                                                                                                                                                                          chromosome 6q24.1-25.2; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Page 14; 21pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 85.1%;
Best Local Similarity 87.8%;
Matches 231; Conservative
                                                                                                                                                                                                                                                                                                                                                                    24-AUG-2001; 2001EP-0250307.
                                                                                                                                                                                                                                                                                                                                                                                                      25-SEP-2000; 2000DE-1048626.
                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-2000; 2000DB-1058907.
19-DEC-2000; 2000DB-1064906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 variant 2 of the invention.
                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SCHD ) SCHERING AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002-332210/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAL46000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and antibodies
                                                                                                                                                                                                                                                                                                        EP1191035-A2.
                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                            08-AUG-2002
                                                                                                                                                                                                                                                                                                                                        27-MAR-2002,
                                                            AA017381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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RESULT 11
                  AA017381
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The present invention relates to a new polynucleotide that encodes a soluble protein which binds to interleukin (IL)-TIF/IL-22 (also referred soluble protein which binds to interleukin (IL)-TIF/IL-22 (also referred to as IL-22BP), where the complementary sequence of the invention hybridises under stringent conditions to a nucleotide sequence of 2271 or 2366 base pairs, as given in the specification. The molecules of the Invention are useful for inhibiting (antagonising) effect of IL-TIF/IL-22 on a cell, for determining whether IL-TIF/IL-22 is present in a sample, for inhibiting binding of IL-TIF/IL-22 to a binding partner, preferably in vitro, and for obtaining an antibody molecule specific for the soluble protein of the invention, from a population or panel of antibody molecules of diverse binding specificity. The soluble protein is further useful in manufacture of a medicament for treating an IL-22 mediated fragment of IL-TIF/IL-22 or the soluble protein, that modulates binding of the soluble protein, that modulates binding of the soluble protein to IL-TIF/IL-22, where the agent identified is used in the manufacture of medicament for treating IL-TIF/IL-22 mediated disorder. The antibody is useful for determining presence of the soluble protein, where the antibody is detectably labelled. The present amino acid sequence represents the human IL-TIF/IL-22 binding protein #1 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide and polypeptide of soluble protein which binds to interleukin-TIF/IL-22 useful for inhibiting effect of IL-TIF/IL-22 on a
                                                                                                                                                                                                                                                                                                 Human, soluble protein, interleukin-TIF/IL-22; IL-TIF/IL-22; IL-22BP;
IL-TIF/IL-22 antagoniet.
                                                                                                                                                                                                                                                         Human IL-TIF/IL-22 binding protein #1.
                           209 AEIYQPMLDRRSQRSEERCVBIP 231
                                                                                                                                        Ä
  241 AEIYOPMLDRRSQRSEERCVEIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 14; Page 39; 42pp; English.
                                                                                                                                    AAU80000 standard; Protein; 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LUDW-) LUDWIG INST CANCER RES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-SEP-2001; 2001WO-US29576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-SEP-2000; 2000US-234583P.
                                                                                                                                                                                                                   15-JUL-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                    WO200224912-A2.
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-2002
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                                                                                                                                                                            AAU80000;
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MMPKHCFLGFLISFFLIGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALIGNSSVY 32; Length 231; Indels Score 1218; DB 23; Pred. No. 1.5e-113; 0; Mismatches 0; tch 85.1%; al Similarity 87.8%; 231; Conservative Query Match Best Local S: Matches 231 -

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PNLPYRYQKEKNVSIEDYYELLYRVPIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVV 208

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PNLPYRYOKEKNVSIEDYYELLYRVFIINNSLEKEOKVYEGAHRAVEIEALTPHSSYCVV

231 AA;

Sequence

the invention.

FVQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDL 120

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Gaps

Indels 32;

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MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY 60

MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY

TSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHA 180

TSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHA 148

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61 FVQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune disorder; haematopotetic disorder; inflammation; arthritis; Parkinson's disease; Huntington's chorea; schizophrenia; antlarrhythmic; multiple sclerosis; Alzheimer's disease; analgeeic; cardiant; asthma; ischaemia; stroke; AlDS; bone disease; atherosclerosis; brain disorder; depression; cardiovascular disease; atherosclerosis; brain disorder; respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder; type II diabetes mellitus; skeletal muscle disorder; immunosuppressive; hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease; nootropic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;
                                                                                             This invention relates to the cDNA and protein sequences of novel secreted and transmembrane polypeptides FRO polypeptides. The invention also comprises a method for producing the proteins of the invention by recombinant means and antibodies specific for the protein of the invention. The antibody may be used for detecting the FRO proteins of the invention and may be used to modify their activity. To isolate the full-length FRO cDNA or to isolate other cDNA its construct hybridisation probes for mapping the gene which encodes that FRO and for genetic analysis of individuals with genetic disorders, in assays to identify other proteins or molecules involved in binding in assays.
                                                                                                                                                                                                                                                                                                                                       reaction, to generate transgenic animals or knock-out animals which in turn are useful in the development and screening of therapeutically useful reagents, for chromosome identification, and tissue typing. The PRO polypeptides are useful in gene therapy, and as molecular weight markers for protein electrophoresis purposes. The sequences may also be used to detect overexpression on PRO polypeptides in cancerous tumours and for screening for differentially expressed genes using microarray technology. The present sequence represents a human PRO protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PVQYKI -----YGQRQWKNKEDCWGTQELSCDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVWNITQVNGSLLVILHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNPHNILQWQPGRALTGNSSVY
  chromosome identification, tissue typing, or individuals with genetic disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, therapy, wound healing disorder, vaccine, cancer, infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cytokine receptor protein, sbg456548CytoRa #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1218; DB 23;
Pred. No. 1.5e-113;
0; Mismatches 0;
                                                               Claim 11; Figure 114; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 AEIYQPMLDRRSQRSEERCVEIP 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEIYOPMLDRRSQRSEERCVEIP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE17320 standard; Protein; 231 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 85.1%;
Best Local Similarity 87.8%;
Matches 231; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
  useful in gene therapy,
for genetic analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
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AAE17320
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                                                                                                                                                               TSETSDIĢEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVNNITQVNGSLLVILHA 148
                                                                                                                                                                                                          PNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVV 240
                                                                                                                                                                                                                                   PNLPYRYQKSKAVVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVV 208
                                        PVOYKIMFSCSMKSSHOKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDL 120
MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY 60
                                                                               ------YGQRQWKNKEDCWGTQELSCDL
                                                                                                                      TSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
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Wood WI, Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; PRO; secreted protein; transmembrane protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Filvaroff E, Goddard A, Stephan J, Watanabe CK,
                                                                                                                                                                                                                                                                                              AEIYOPMLDRRSQRSEERCVEIP 263
                                                                                                                                                                                                                                                                                                                         ARIYQPMLDRRSQRSEERCVEIP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG34086 standard; Protein; 231 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genetic disorder; tumour; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JAN-2001; 2001US-262150P.
25-JAN-2001; 2001US-264395P.
02-FEB-2001; 2001US-26421P.
09-FEB-2001; 2001US-267623P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-JAN-2001; 2001US-261878P.
16-JAN-2001; 2001US-261910P.
16-JAN-2001; 2001US-261939P.
16-JAN-2001; 2001US-262150P.
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2001US-280982P
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                                                                               FVQYKI -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Pro peptide #57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eaton DL,
Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-362426/39
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03-APR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gurney AL,
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RESULT 13 ABG34086

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208

180 148

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32; Gaps

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The invention relates to secreted and membrane-associated polypeptides and polynucleotides. The sequences of the invention are useful in diagnostic assays for detecting diseases associated with inappropriate activity or levels of these polynucleotides, and in identifying their agonists and antagonists that are potentially useful in therapy. The sequences of the invention are useful as vaccines for inducing timmunological response. The sequences of the invention are useful for treating cancers, infections, autoimmune disorders, hematopoietic cimmunological response. The sequences of the invention are useful for treating cancers, infections, autoimmune disorders, hematopoietic cimmunological response. The sequences of the invention are useful for treating cancers, infections, alsease, Huntington's choice, multiple sclerosis, bullosa, Parkinson's disease, Huntington's choice, multiple sclerosis, viral and bacterial infections, Alzheimer's disease, transplant rejection, allergies, schizophrenia, spay1432FRO3-associated disorders, respiratory disease including parasupranuclear palsy, myotonic dystrophy, depression, anxiety disorders and sleep disorders, cardiovascular disease including parasupranuclear palsy, myotonic dystrophy, depression, anxiety disorders and sleep disorders, cardiovascular ceptical including chronic obstruction diseases including chronic obstruction, creptical muscle disorders including hypoertolesterolaemia, hypertriglyceridaemia, cirrhosis, viral and non-viral hepatitis, type II diabetes mellitus, renal disease including acute and chronic renal failure, glomerulonephritis, gastrointestinal diseases including hypoersplenism, contendintis, gastrointestinal diseases including hypoersplenism, hodskin's disease and malignant lymphoma, testicular cancer, male reproductive disease and malignant lymphoma, testicular cancer, male reproductive disease including lower respiratory and rendintis; human over honer or man en renoice is human over or man en entering sections or exproductive diseases including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel secreted and membrane-associated polypeptides and polynucleotides useful for preventing, ameliorating or correcting dysfunction or disease including diabetes, cancer, hypertension and growth
haemostatic, vulnerary, anticonvulsant, antirheumatic, neuroprotectiv nephrotropic, hypotensive, vasotropic, cytostatic, cerebroprotective, allergy, cytokine receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                              Martensen SA;
Xie Q, Rizni SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.1%; Score 1218; DB 23; Length 231; 87.8%; Pred. No. 1.5e-113; ive 0; Mismatches 0; Indels 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is human cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                         , Kabnic KS, Lai Y,
Strum JC, Xiang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 132-133; 138pp; English
                                                                                                                                                                                                                                                                                                                                  SMITHKLINE BEECHAM CORP.
SMITHKLINE BEECHAM PLC.
GLAXO GROUP LTD.
                                                                                                                                                                                                                                                            22-JUN-2000; 2000US-213156P.
22-JUN-2000; 2000US-213161P.
                                                                                                                                                                                                                  22-JUN-2001; 2001WO-US19929
                                                                                                                                                                                                                                                                                                                                                                                                                         Cogswell JP,
Smith RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-139783/18.
N-PSDB; AAD27815.
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les 231; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 AA;
                                                                                                                              WO200198342-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  abnormalities
                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                           P,
PR,
                                                                                                                                                                                                                                                                                                                              (SMIK) (SMIK) (SMIK) (GLAX) (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Murdock
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180
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                                                                                                                           PNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVV 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to cytokine receptor polypeptide, Zcytor16. The polypeptide is useful in modulating the immune system by binding Zcytor16 ligand and thus preventing the binding of the ligand with endogenous
                       88
                                                                                                                                                                                                                                                                                                                                                                              Human; cytokine receptor; Zcytor16; immune function; autoimmune disease; inflammatory bowel disease; ulcerative colitis; Crohn's disease; asthma; arthritis; psoriasis; endotoxaemia; septicaemia; toxic shock syndrome; infectious disease; cancer; diabetes; renal dysfunction; pancreatitis; spontaneous abortion; placental health; gene therapy; nephrotropic; chromosome 6q23-q24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune or
                                                                   TSETSDIQEPYYGRVRAASAGSYSEWSWTPRFTPWWETKIDPPVMNITQVNGSLLVILHA
                                                                                                          PNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVV
FVQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDL
                          -----YGQRQWKNKBDCWGTQELSCDL
                                                     121 TSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tor16 polypeptide useful for treating or detecting autoimmu
atory diseases, e.g. inflammatory bowel disease, arthritis,
diabetes, cancer, psoriasis, endotoxemia, septicemia, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hughes SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Mature human Zcytor16 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Fibronectin III domain II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Fibronectin III domain I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kindsvogel W, Chen Z,
                                                                                                                                                                                                                                                                                                                                                     Human cytokine receptor, Zcytor16 protein.
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/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 233-234; 268pp; English.
                                                                                                                                                                263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                 AAE30826 standard; Protein; 231 AA.
                                                                                                                                                                                         AEIYOPMLDRRSQRSEERCVEIP
                                                                                                                                                                241 AEIYQPMLDRRSQRSEERCVEIP
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128..131
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/note= "F
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                         61 FVQYKI ----
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inflammatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
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1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY

Conservative

Matches

8

32;

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2cytor16 receptor. It is useful for studying human inflammation or immune
                                function, or for treating autoimmune or inflammatory diseases such as inflammatory bowel disease, ulcerative colitis, Crohn's disease, arthritis, psoriasis, endotoxaemia, septicaemia, toxic shock syndrome or infectious disease, asthma, cancer, diabetes, renal dysfunctions or infectious disease, asthma, cancer, diabetes, renal dysfunctions or pancreatitis or in assessing therapeutic aspects of ILTIF, chemical therapeutics, anti-ILTIF antibodies, anti-Zcycoris antibodies or Zcytoris soluble receptors. The nucleic acid molecule and the antibody are useful as probes in detecting gene expression and gene structure, such as in the diagnosis and/or prevention of spontaneous abortions or in monitoring placental health and function. The invention is useful in gene therapy. The present sequence is human Zcytoris protein. Zcytoris gene is located on chromosome 6q23-q24.
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231 AA; Sequence

181 PNLPYRYOKEKNVSIEDYYELLYRVFIINNSLEKEOKVYEGAHRAVEIEALTPHSSYCVV 240 61 FVQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDL 120 121 TSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHA 180 89 TSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHA 148 149 PNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVV 208 1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY 60 61 FVQYKI-----YGQRQWKNKEDCWGTQELSCDL 88 Gaps 32; Length 231; Indels Query Match 85.1%; Score 1218; DB 24; Best Local Similarity 87.8%; Pred. No. 1.5e-113; Matches 231; Conservative 0; Mismatches 0; 241 AEIYOPMLDRRSQRSEERCVEIP 263 209 AEIYQPMLDRRSQRSEERCVEIP 231 ď ઠે 셤 Š 셤 Š 임 ò 셤

Search completed: December 12, 2003, 12:25:33 Job time : 67.8644 secs

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COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: STEM COMPACTABLE DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY, AGENT INFORMATION:
NAME: LUUN, PAUL G
REGISTRATION NUMBER: 32,743
REGISTRATION NUMBER: 32,743
REGISTRATION NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jelhoberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Adams, Robyn L.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1201 Bastlake Avenue Ba CITY: Seattle STATE: WA COUNTRY: USA
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Patent No. 5945511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 221 amino acide
TYPE: amino acid
STRANDEDNESS: single
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TELEX:
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MOLECULE TYPE: protein

PRAGMENT TYPE: internal
US-08-943-087-52
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App I
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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US-08-110-683-4
US-08-472-097-4
US-08-472-097-4
US-09-419-672-4
US-07-683-682B-4
US-07-683-682B-4
US-08-311-77-2
US-08-311-77-2
US-08-463-931-6
US-08-463-931-6
US-08-463-931-6
US-08-463-931-6
US-08-463-931-2
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90; Indels

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33; Mismatches
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TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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   74; Conservative
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Kho, Choon J.
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MEDIUM TYPE: Diskette
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FRAGMENT TYPE: internal
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                                                                                                                                                            47 -----YĞÇKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIMGTKCSKWAES 97
                                                                      30 KPQRVQPQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 89
                                                                                         34; Gaps
                                                                                                                                                                                                                                                                                     NNSLEKEOKVYEGAHRAVEIEALTPHSSYCVVAEIYOPMLDRRSQRSEERC 259
                                                                                                                                                                                                                                                                                                          Length 221;
 Length 221;
                                     90; Indels
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Pred. No. 2.2e-27;
Query Match 21.7%; Score 311; DB 2; Best Local Similarity 32.0%; Pred. No. 1.7e-27; Matches 74; Conservative 33; Mismatches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FSESEG for Windows Version 2.0
SOFTWARE: TSESEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Whitmore, Theodore E. APPLICANT: Farrah, Theresa M. TITLE OF INVENTION: CYTOKINE RECEPTOR NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 50, Application US/08943087
Patent No. 5945511
GENERAL INFORMATION:
APPLICANT: No. Choon J.
APPLICANT: Adms, Robyn L.
APPLICANT: Mintmore, Theodore E.
APPLICANT: Parrah, Theresa M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
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32.0%;
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LENGTH: 221 amino acids
TYPE: amino acid
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TELEFAX: 206-442-6678
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INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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Best Local Similarity
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FRAGMENT TYPE:
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STATE:
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                                                                                                                                                    47 ------YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 97
30 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 89
                                                                                                                                                                                                                                                                                                                                               209 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 259
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APPLICANT: Adams, Robyn L.
APPLICANT: Mitemore, Theodore E.
APPLICANT: Farrah, Theresa M.
ATILE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: LUNN. Paul
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 56, Application US/08943087
Patent No. 5945511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue
CITY: Seattle
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127 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 186
                                       90 PPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSWT 149
                                                                             ------YGQKKWLNKSECRNINRTYCDLSAETSDYBHQYYAKVKAIWGTKCSKWAES 126
                                                                                                                    150 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII
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                                                                                                                                                                                                 209 NNSLEKEOKVYEGAHRAVEIEALTPHSSYCVVAEIYOPMLDRRSORSEERC 259
39 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI-
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SUFTWARE: FatleSRO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
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APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore Theedex B.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
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CLASSIPTICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FRB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/08943087
Patent No. 5945511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-627
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                     Lok, Si
Kho, Choon J.
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TELEX:
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MOLECULE TYPE:
FRAGMENT TYPE:
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                                                                               90 PPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 149
                                                                                                                                                                                     150 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 208
                                                                                                      -----YGQKKWINKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGSKCSKWAES 97
    KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 89
                                                                                                                                                                                                                                                                  209 NNSLEKEQKVYEGAHRAVEIBALTPHSSYCVVAEIYOPMLDRRSQRSEERC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 2; Length 553; 9.3e-27;
                                       10 KPANITFLSINMKNVLÓWTPPEGLOGVKVTÝTVOÝFÍ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
ODERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.6%; Score 310; DB 32.0%; Pred. No. 9.3e-tive 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSER: ZymoGenetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 96-24C1
FELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08943087
Patent No. 5945511
GENBRAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : ZymoGenetics, Inc.
1201 Eastlake Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jelmberg, Anna C.
Adams, Robyn L.
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                  Lok, Si
Kho, Choon J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 32.09
Matches 74; Conservative
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internal
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seattle
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FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                US-08-943-087-2
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30 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 89
Query Match 21.6%; Score 310; DB 2; Length 553; Best Local Similarity 32.0%; Pred. No. 9.3e-27; Matches 74; Conservative 33; Mismatches 90; Indels
                                                                                                                                                                                          39 KPANITFLSINMKAVLQWTPPEGLQGVKVTYTVQYFI-----
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30 KPORVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 89

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-----YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 126
                                              150 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 208
                                                                              127 GREYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSWT 149
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                                                                                                                               209 INSLEKECKVYEGAHRAVEIEALTPHSSYCVVAEIYOPMLDRRSGRSEERC 259
                                                                                                                                                          39 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI------
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OPERATING SYSTEM: DOS
SOFTWARE: FASTENCY FOR Windows Version 2.0
SURRENT APPLICATION DATA: Windows Version 2.0
APPLICATION NUMBER: US/08/943,087
FILING DATE: DATE: DATA: MAPPLICATION: S36
PRIOR APPLICATION: DATA: APPLICATION NUMBER: 08/803,305
ATTORNEY/AGENT INFORMATION:
NAME: Luun, Paul G
REGISTRATION NUMBER: 32,743
***COMPUTER: LUUN, Paul G
REGISTRATION NUMBER: 96-24C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
21.6%; Score 310; DB 2;
Best Local Similarity 32.0%; Pred. No. 9.3e-27;
Matches 74; Conservative 33; Mismatches 90
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: ZymoGenetics, Inc.
1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                          Sequence 18, Application US/08943087
Patent No. 5945511
                                                                                                                                                                                                                                                                                                                                             Lok, Si
Kho, Choon J.
Jelmberg, Anna C.
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TELECOMMUNICATION INFORMATION
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 553 amino acida
TYPE: amino acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
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APPLICANT: Lok, S
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                          -----YGQKKWINKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 126
90 FPGCRTLAKYGOROWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 149
                                                                                                         127 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 186
                                                                                150 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 208
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                                                                                                                                                                                              187 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 236
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                                                                                                                                                                209 NNSLEKEOKVYEGAHRAVEIEALTPHSSYCVVAEIYOPMLDRRSORSEERC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    th 21.6%; Score 310; DB 2; Length 553; Similarity 32.0%; Pred. No. 9.3e-27; 74; Conservative 33; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION NUMBER: 08/803,305
PRIOR APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
APPLICATION NUMBER: 20-FEB-1997
APPLICATION NUMBER: 32,743
NAME: LUAIN, PAUL G
REGISTRATION NUMBER: 32,743
... PROCESTRATION NUMBER: 96-24C1
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/08943087
Patent No. 5945511
GENERAL INFORMATION:
APPLICANT: LOK, Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                   Lok, Si
Kho, Choon J.
Jelmberg, Anna C.
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein FRAGMENT TYPE: internal
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Matches 74; Conserva
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                          RESULT 6
US-08-943-087-16
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127 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWRRNPEDLPVSMQQIYSNLKYNVSVL 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 -----YGOKKWINKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN
                                             209 NNSLEKECKVYEGAHRAVEIEALTPHSSYCVVAEIYOPMLDRRSORSEERC 259
                                                                      Length 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 KPANITFLSINMKNVLÓWTPPEGLOGVKVTÝTVÓYFÍ-----
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32.0%; Pred. No. 9.3e-27;
iive 33; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SUFTWARE: FRSEUSO for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
                                                                                                                                                                                                                      APPLICANT: LOK, Si
APPLICANT: Kho, Choon J.
APPLICANT: Almberg, Anna C.
APPLICANT: Maintmore, Theodore E.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Watenore, Theodore E.
APPLICANT: Watenore, Theodore E.
APPLICANT: Partarb, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                            B: ZymoGenetics, Inc.
1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: 08/803,305
FILING DATB: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96-24C1
                                                                                                                                                                                          Sequence 22, Application US/08943087
Patent No. 5945511
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           553 amino acids
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Best Local Similarity 32.0%
Matches 74; Conservative
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TELEFAX: 206-442-6678
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION:
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                           127 GRFYPFLETQIGPPEVALTIDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 186
150 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 208
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                                                                                                           187 NTKSNRTWSQCVTNHTLV-LIWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 236
                                                                                  209 NNSLEKEOKVYEGAHRAVEIEALTPHSSYCVVAEIYOPMLDRRSORSEERC 259
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastesc for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
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TITLE OF INVENTION: CYTOKINE RECEPTOR NUMBER OF SEQUENCES: 60
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                             Sequence 20, Application US/08943087
Patent No. 5945511
GENERAL INFORMATION:
APPLICANT: Kho, Choon J.
APPLICANT: Jelmberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Parrah, Theresa M.
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TYPE: amino acid
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Matches 74; Conservative
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FRAGMENT TYPE: internal
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ADDRESSEE: ZymoGenet
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187 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 236
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                                                                                   Sequence 26,
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                      187 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 236
     209 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 553;
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32.0%; Pred. No. 9.3e-27;
tive 33; Mismatches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SUFTWARE: PRESESO for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
                                                                                                                                                                                                                                                                   TITLE OF INVENTION: CYTOKINE RECEPTOR NUMBER OF SEQUENCES: 60 CORRESPONDENCE ADDRESS: ADDRESSE: ZymoGenetics, Inc.
                                                                                                                                                                                                                                                                                                                                        Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
ATILING DATE: 20-FBB-1997
ATTORNEY/AGENT INFORWATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96-24C1
                                                                                                                  Sequence 24, Application US/08943087
Patent No. 5945511
                                                                                                                                                                                                                                       Theodore B.
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ELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                    Jelmberg, Anna C.
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                       Farrah, Theresa
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amino acid
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Kho, Choon J.
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INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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Best Local Simi
Matches 74;
                                                                                                    US-08-943-087-24
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APPLICANT:
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90 FPGCRTLAKYGGRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 149
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                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/943,087 FILLIG DATE:
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                                                                                                   APPLICANT: Kho, Choon J.
APPLICANT: Jelmberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                           1: ZymoGenetics, Inc.
1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFTCATION: 536
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 08/803,305
FILING DATE: 20-FBB-1997
ATTORNEY/AGENT INFORMATION:
                   6, Application US/08943087
5945511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96.
TELECOMMUNICATION:
TELECOMMUNICATION:
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IBM Compatible
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                                                                                     Lok, Si
Kho, Choon J.
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LENGTH: 553 amino acio
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Best Local Similarity
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MOLECULE TYPE:
FRAGMENT TYPE:
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RESULT 11
US-08-943-087-26
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Application US/08943087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.6%; Score 310; DB 2; Length 553; 32.0%; Pred. No. 9.3e-27; tive 33; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
                                                                         CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRAATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                         Sequence 28, Application US/08943087
Patent No. 5945511
GRNERAL INFORMATION:
APPLICANT: LOK, SI
APPLICANT: Kho, Choon J.
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 553 amino acids TYPE: amino acid STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
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Best Local Similarity
Matches 74; Conserva
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                                                                                                                                                                                                                                                          Seattle
                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                      ZIP: 98102
RESULT 12
US-08-943-087-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-943-087-28
                                                                                                                                                                                                                                                        CITY: S
STATE:
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RESULT 13

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90 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

21.6%; Score 310; DB 2; Length 553;
Best Local Similarity 32.0%; Pred. No. 9.3e-27;
Matches 74; Conservative 33; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 KPANITFLSINMKNVLOWTPPEGLOGVKVTYTVOYFI------
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
SUFTWARE: FastERD for Windows Version 2.0
SUFTWAREINT APPLICATION DATE:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REGISTRATION NUMBER: 96-24C1
                                                                                                                                                                                                                STREET: I201 Eastlake Avenue East CTTY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-943-087-32
; Sequence 32, Application US/08943087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6677
TELEFAX: 206-442-6678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 KPANITFLSINMKAVLQWTPPEGLQGVKVTYTVQYFI------75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 21.6%; Score 310; DB 2; Length 553;
Best Local Similarity 32.0%; Pred. No. 9.3e-27;
Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 INSLEKEQKVYEGAHRAVEIEALIPHSSYCVVAEIYQPMLDRRSQRSEERC 259
                                                                                                                                                                                                                                                                                                                 ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastESG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
               GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Mitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPENDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
                                                                                                                                                                                    STATE: WA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PLING DATE:
FILING DATE:
FILING DATE:
701-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REBERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELECHUNE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96-24C1
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; Sequence 34, Application US/08943087
Patent No. 5945511
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
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TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
Patent No. 5945511
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90 FPGCRTLAKYGQRQWKWKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSWT 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 21.6%; Score 310; DB 2; Length 553; Best Local Similarity 32.0%; Pred. No. 9.3e-27; Matches 74; Conservative 33; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
APPLICANT: Kho, Choon J.
APPLICANT: Jelmberg, Anna C.
APPLICANT: Jelmberg, Anna C.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrarh, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS: 2ymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: December 12, 2003, 12:16:32 Job time : 26.8542 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILLING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION BATA:
APPLICATION NUMBER: 00/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFREENCE/DOCKET NUMBER: 96-24C1
TELEPHONE: 206-442-6627
TELEPHONE: 206-442-6679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 34: SEQUENCE CHARACTERISTICS: LENGTH: 553 amino acids TYPE: amino acid strandedness; single
                                                                                                                                                                                                                                                                                                                                                                         E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                   Seattle
                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                          98102
                                                                                                                                                                                                                                                                           STATE: WA
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24.0712
time
; Search time 24.07
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12:2
2003,
12,
December 12, 2003, 12:23:03; Search time 24.0712 Second
Run on:

(without alignments) 1050.732 Million cell updates/sec Perfect score: 1432 Sequence: 1 MMPKHCFLGFLISFFLTGVAYQPMLDRRSQRSEBRCVEIP 263 Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283308 segs, 96168682 residues

Searched:

283308

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. PIR 76:* 1: pir1:* 2: pir2:* 3: pir3:* 1: pir4:*

tissue factor prec interferon alpha r interferon recepto interleukin-10 rec cytokine receptor tissue factor prec interferon alpha/b interferon alpha/b tissue factor prec interferon gamma r tissue factor prec interferon gamma r interferon alpha-b interferon alpha/b interferon recepto interferon gamma r structural polypro structural polypro Kallmann syndrome probable phospholi probable transcrip probable transcrip RNA binding protel interleukin-10 rec structural polypro hypothetical prote interferon gamma r ribonucleoside-dip Kallmann syndrome Description SUMMARIES A49667 KEHU3 CG311 JCG311 ISG115 A47003 A47003 A47003 A47003 A475283 A475283 KFMS3 A41555 A41595 A41295 A54295 SS9501 VHWV S42462 A47222 B47222 S37136 T02748 A34368 % Query Match Length DB 164.5 163 158 156 155 1149.5 1138.5 1134.5 1132.5 110.5 110.5 110.5 110.5 110.5 110.5 110.5 Score 87.5 87.5 87 Result No.

gene B9R protein - hypothetical prote	hemolysin export s	hypothetical prote	sensor protein kin	hypothetical prote	hypothetical prote	calpain (EC 3.4.22	structural polypro	hemolysin secretio	beta-glucosidase h	IL-13Ralpha 1 prot	choline kinase (EC	hypothetical prote	probable exported	hypothetical prote
136855 T02623	LEECD	T15972	B86834	T25489	T21423	S57196	VHWVN2	S10058	T02128	JC7773	A32034	T01041	AF0911	AG2311
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266 479	478	650	456	430	564	810	1247	478	527	426	582	884	1266	335
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8 83	82.5	82.5	81.5	81	81	81	81	80.5	80.5	80	80	90	79.5	79

ALIGNMENTS

RESULT 1 A49667 interleukin-10 receptor - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;State 102-Uul-1996 #sequence_revision 02-Uul-1996 #text_change 28-Jul-2000 C;Accession: A49667 R;Ho, A.S.; Liu, Y.; Khan, T.A.; Hsu, D.H.; Bazan, J.F.; Moore, K.W. Proc. Natl. Acad. Sci. U.S.A. 90, 11267-1121, 1993 A;Title: A receptor for interleukin 10 is related to interferon receptors. A;Reference number: A49667; MUID:94068585; PRID:8248239 A;Residues: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-575 kES> A;Coss references: GB:L12120; NID:9437615; PIDN:AAA16156.1; PID:g437616 C;Genetics: A;Gene: 1110r C;Superfamily: interleukin-10 receptor IL10R C;Superfamily: interleukin-10 receptor IL10R C;Superfamily: interleukin-10 receptor IL10R C;Superfamily: interleukin-10 receptor IL10R C;Superfamily: interleukin-10 receptor C;Superfa		150	QY 177 ILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKYYEGAHRAVEIEALT- 	Qy 233PHSSYCVVAEIYQPMLDRRSQRSEERCVEI 262
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16;

9

28

ETS 125

LLV 176

Fri 90

IYG 144

232

FTL 194

KESULT 2
KPHU3
Lissue factor precursor [validated] - human
NyAlternate names: coagulation factor III
NyAlternate names: coagulation factor III
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 08-Dec-2000
C;Accession: A43645; A47574; A28320; A29662; A29672; A29008

217

---DWKSK--CFYTTDTECDLTDEIVKDVKO 101

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A;Title: Specific antiviral activities of the human alpha interferons are determined A;Reference number: $27387; MUID:93076908; PMID:1446745
                         SMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSE-TSDIQE 129
                                                                                                                                                                                 102 TYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPTIQSFEQVGTKVNVTVED 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rilim, J.K.; Langer, J.A.
Biochim. Biophys. Acta 1173, 314-319, 1993
A;Title: Cloning and characterization of a bovine alpha interferon receptor.
A;Reference number: S33770; MUD:93305725; PMID:8318540
A;Accession: S33770
A;Scatus: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interferon alpha receptor type 1 precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Pate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
                                                                                                                                                 130 PYYGRV-----RAASAGSYSE--WSMTPRFTPWWETKI-DPPVMNITQVNGSLLVILHA
                                                                                                                                                                                                                                                                  181 PNLPYRYQKEKNVSIEDYY'--ELLYRVFIINNSLEKEOKVYEGAHR-AVEIEALTPHSSY
                                                                                                                                                                                                                                                                                                               A;Residues: 1-560 <MOU>
A;Cross-references: EMBL:X68443; NID:g431; PIDN:CAA48484.1;
A;Experimental source: MDBK cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: S27387; S33770 — R;Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, FEBS Lett. 313, 255-259, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary, nucleic acid sequence not shown A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                            C--VVAEIYOPMLDRRSORSEERCV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                CFSVQAVIPSRTVNRKSTDSPVECM 242
                                                                                       STKSG---
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R;Mackman, N.; Morrissey, J.H.; Fowler, B.; Edgington, T.S.
Biochemistry 28, 1752-1762, 1989
A;Attle: Complete sequence of the human tissue factor gene, a highly regulated cellular A;Accession: A43645, MUID: 99247359; PMID: 2719931
A;Accession: A43645
A;Access-reference: GB-102846, MID: 9339505; PIDN: AA661152.1; PID: 9339506
A;Fibher; K.L.; Gorman, C.M.; Vehar, G.A.; O'Brien, D.P.; Lawn, R.M.
A;Reference number: A47574; MUID: 98100453; PMID: 3424266
A;Attle: Cloning and expression of human tissue factor conva.
A;Reference number: A47574; MUID: 98100453; PMID: 3424266
A;Accession: A47574; MUID: 98100453; PMID: 3037566
A;Accession: A28326
A;Accession: A28326
A;Accession: A28326
A;Accession: A2962; MUID: 97260946; PMID: 3037536
A;Accession: A2962
A;Accession
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A; Residues: 1-259, A', 261-295 <SCA>
A; Residues: 1-259, A', 261-295 <SCA>
A; Residues: 1-259, A', 261-295 <SCA>
A; Cross-references: GB.MH6553; NID: 9339503; PIDN: AAA61151.1; PID: 9339504
B; Dechemistry 27, 4227-4231, 1988
A; Title: Human tissue factor contains thioester-linked palmitate and stearate on the cyt
A; Cherence number: A37422; MUID: 99000604; PMID: 3166978
A; Contents: annotation; disulfide bonds and fatty acid binding site
C; Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
C; Comment: Expression of tissue factor can be induced in a variety of tissues by certain
C; Genetics:
A; Gene: GDB: F3
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Best Local S
Matches 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --------KWKQIPNCENVTSTHCVFPREVSS-RGIYYVRVRASNGN 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 SYSEWSMIPRFIPWWEIKIDPPVMNITQV-NGSLLVILHAPNLPYRYQKEKNVSIEDYYE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     314 GISFWSEEKEFNTEMKTIIFPPVISVKSVTDDSLHVSVGAS-----EESENMSVNQLYP 367
                                                                                                                                                                                                                                                                                                                                                                                                                             81
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C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPML--DRRSQRS 255
                                                                                                                                                                                                                                                                                                                                                                                                                         TQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TERHKVPSPENIQINADNQIYVLKWD----YPYENATFQAQWLRAFFKKIPGNHSD---
A Residues: 1-421,'V', 423-560 <LIM>
A; Cross-references: EMBL:L06320; NID:g163187; PIDN:AAA02571.1; PID:g163188
A; Experimental source: lung
C; Keywords: antiviral; cytokine receptor; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-560/Product: interferon alpha receptor type 1 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42;
                                                                                                                                                                                                                                                                     11.0%; Score 158; DB 2; Length 560; 24.1%; Pred. No. 4.9e-06;
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 24.1%; Pred. No. 4.9e-uo;
Matches 57; Conservative 38; Mismatches 100; Indels
Matches 57; Conservative 38; Mismatches 100; Indels
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13;

Gaps

58;

Indels

45; Mismatches 100;

Conservative

62;

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11 LISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSC 70

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A; Status: preliminary
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                                                                       mouse proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VQYKIMFS----CSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 CDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVI 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 LHAPNLPYRYOKE-----KNVSIEDYYELLYRV-FIINNSLEKEQKVYEGAHRAVEIEA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 FVQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDL 120
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                                                                                                                                                                                                                                                                                                                        6 CFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQ----PGRALTGNSSVYF 61
                                                                                                                                                                                                                                                                                                                                                                     CVAGWLGGFLLVPALGMIP-----PPEKVRMNSVNFKNILQWEVPAFPKTNLT----FT 53
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C;Date: 02-uul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Jul-2000
C;Dates: 01-1996 #sequence_revision 02-Jul-1996 #text_change 28-Jul-2000
C;Accession: 155215
R;Liu, Y.; Wei, S.H.; Ho, A.S.; de Waal Malefyt, R.; Moore, K.W.
J. Immunol. 152, 1821-1829, 1994
A;Title: Expression cloning and characterization of a human IL-10 receptor.
A;Reference number: 156215; MUID:94165477; PMID:8120391
                                                                                                                                                                                                                                                                                    Gaps
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C;Accession: JC6311
R;Gibbs, V.C.; Pennica, D.
Gene 186, 97-101, 1997
A;Title: CRF2-4:isolation of cDNA clones encoding the human and 1
A;Reference number: JC6311; MUID:97199375; PMID:9047351
A;Status: preliminary
A;Redule type: mRNA
A;Residues: 1-349 cGIB>
                                                                                                                                                                                                                                        Length 349;
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                                                                                                                                                                                                                                   Query Match
10.9%; Score 156; DB 2; Length 349
Best Local Similarity 26.8%; Pred. No. 4e-06;
Matches 72; Conservative 30; Mismatches 89; Indels
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A;Residues: 1-578 <RES>
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A,Cross-references: GDB:330958, OMIM:146933
A,Map position: 11q23.3-11q23.3
C,Superfamily: interleukin-10 receptor IL10R
C,Keywords: cytokine receptor
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Matches 64; Conservative
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cytokine receptor family class II protein CRF2-4 precursor - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A47003; G01418
R;Lutfalla, G.; Gardiner, K.; Uze, G.
R;Lutfalla, G.; Gardiner, K.; Uze, G.
A;Title: A new member of the cytokine receptor gene family maps on chromosome 21 at less the family maps on chromosome 21 at less the family maps on chromosome 21 at less than the cytokine receptor gene family maps on chromosome 21 at less than the family maps on chromosome 21 at less than the cytokine receptor gene family maps on chromosome 21 at less than the cytokine receptor gene family maps on chromosome 21 at less than the cytokine receptor gene family maps on chromosome 21 at less than the cytokine receptor gene family maps on chromosome 21 at less than the cytokine receptor gene family maps on chromosome 21 at less than the cytokine receptor gene family maps on chromosome 21 at less than the cytokine receptor gene family maps on chromosome 21 at less than the cytokine receptor gene family maps on chromosome 21 at less than the cytokine receptor gene family maps on chromosome 21 at less than the cytokine receptor gene family maps on chromosome 21 at less than the cytokine receptor gene family maps on chromosome 21 at less than the cytokine receptor gene family maps on chromosome 21 at less than the cytokine receptor gene family maps on chromosome 21 at less than the cytokine receptor gene family maps on chromosome 21 at less than the cytokine receptor gene family maps on chromosome 21 at less than the cytokine receptor gene family maps on chromosome 21 at less than the cytokine receptor gene family maps on chromosome 21 at less than the cytokine receptor gene family maps on chromosome 21 at less than the cytokine receptor gene family maps on chromosome 21 at less than the cytokine receptor gene family maps on chromosome 21 at less than the cytokine receptor gene family maps on chromosome 21 at less than the cytokine receptor gene family maps on chr
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                                                                   173 SLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVF-IINNSLEKEQKVYEGAHRAVEIEAL 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 EWSMIPRFIPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYO--KEKNVSIEDYYELL 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 ------YGDHTLRYRAEFADEHS 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 PQRVQFQSRNFHNILLQWQPGRALTGN--SSVYFVQYKIMFSCSMKSSHQKPSGCWQHISC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Visible factor precursor - bovine

NyAlternate names: coagulation factor III

C)Species: Bos primigenius taurus (cattle)

C)Accession: JQ1319

R)Takayenoki, Y.; Muta, T.; Miyata, T.; Iwanaga, S.
Biochem. Blophys. Res. Commun. 181, 1145-1150, 1991

A;Title: CDNA and amino acid sequences of bovine tissue factor.

A;Reference number: JQ1319; MUID:92109720; PMID:1764065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 YRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: mRNA
A,Residues: 1-325 <LUT>
A,Cross-references: GB:Z17227; NID:g393378; PIDN:CAA78933.1; PID:g393379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59;
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                                                                                                                                                                                                                              232 TPHSS----YCVVAEIYOPMLDRRSQR---SEERCVEI 262
                                                                                                                                                                                                                                                                                                  A;Residues: 1-123,'D',125-269,'VGRME' <LU2>
A;Cross-references: EMBL:U08988; NID:9571295; PID:9571296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
10.4%; Score 149.5; DB 2
Best Local Similarity 24.1%; Pred. No. 1.4e-05;
Matches 57; Conservative 32; Mismatches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Lutfalla, G. submitted to the EMBL Data Library, April 1994 Wheference number: G06935 A;Accession: G01418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A)Gene: GDB:CRFB4; CRF2-4
A)Cross-references: GDB:138168; OMIM:123889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 21q; 21q22.1-21q22.2
A;Introns: 17/1; 58/2; 111/1; 166/3; 216/1
C;Keywords: transmembrane protein
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F;437-455/Domain: transmembrane #status predicted <TRN2>
F;50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QWLHAFLKRNPGNH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 IY--QPMLDRRSQRSEERC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHIMDEKLNKSSVFSDAVC 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 265-375 < RE4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 118-125 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Residues: 397-424 <RE5>
                                                                                                        Query Match
Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                                                                                                                                                                                  217 PVHCI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: 148425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: A45283
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Cyncession: A32694, Mulb:90124632, PMID:2153461
A;Reference number: A32694, Mulb:90124632, PMID:2153461
A;Residues: 1-557 cyncered: A;Rolecule type: mRNA
A;Residues: 1-557 cyncered: GB:J03171, NID:g184645, PIDN:AAA52730.1, PID:g306914
A;Molecule type: MRNA
A;Residues: 1-557 cyncered: GB:J03171, NID:g184645, PIDN:AAA52730.1, PID:g306914
A;Description: The structuree of the human interferon alpha/beta receptor gene.
A;Reference number: S17112
A;Accession: S17112
A;Accession: S17112
A;Residues: 1-16, A, 18-329, VV, 343-557 cynr>
A;Residues: 1-16, A, 18-329, VV, 343-557 cynr>
C;Genetics: Cyncered centered center
                                                                        ; Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane; 135/Domain: signal sequence #status predicted <SIG>
7,36-292/Product: tissue factor #status experimental <MAT>
7,36-292/Product: tissue factor #status predicted <TM>
7,36-292/Domain: extracellular #status predicted <TM>
7,279-292/Domain: transmembrane #status predicted <TM>
7,373-292/Domain: intracellular #status predicted <IMT>
7,31,31/Binding site: carbobydrate (Asn) (covalent) #status predicted 
7,318,134/Binding site: carbobydrate (Thr) (covalent) #status predicted 
7,318,134/Binding site: carbobydrate (Thr) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 SMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSE-TSDIQE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----PRLG--NWKNK--CFYTTNTECDVIDEIVKNVRE 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 PYYGRVRAASAGSYSE----WSMTPRFTPWWETKI-DPPVMNITQVNGSLLVILHAPNL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 TYLARVLSYPADISSSTVEPPFINSPEFTPYLETNLGOPTIOSFEQUGIKLNVTVODART 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 PYRYOKEKNVSIEDYY--ELLYRVFIINNSLEKEOKVYEGAHR-AVEIEALTPHSSYC-- 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 LVR-ANSAFLSLRDVFGKDLNYTLYYWKASSTGKKKATTNTNGFLIDVD---KGENYCFH 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 LISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71
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A;Cross-references: GDB:120078; OMIM:107450
A;Rimap position: 21q22.1-21q22.1
A;Introns: 26/1; 6/2; 126/1; 7/2; 226/1; 263/2; 342/1; 381/3; 432/1; 480/3
C;Keywords: cytokine receptor; glycoprotein, transmembrane protein
P;1-21/Domain: transmembrane #status predicted <TRN1>
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C;Species: Homo sapiens (man)
C;Date: 22.Jun-1990 #sequence_revision 22-Jun-1990 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 LFGLVLIQGAGVAGTTDVVVAYNITWKSTNFKTILEWEPKPI----NHVYTVQIS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55; Gaps
                                Residues: 1-292 <TAK>
Cross-references: GB:S74147; NID:g241438; PIDN:AAB20755.1; PID:g241439
Experimental source: adrenal gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 9.7%; Score 138.5; DB 1; Best Local Similarity 22.6%; Pred. No. 0.00011; Matches 59; Conservative 43; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 VVAEIYQPMLDRRSQRSEERC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | | | ::::| ::|
VQAVILSRRVNQKSPESPIKC 238
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A;Reference number: 148423; MUID:95047447; PMID:7958966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interferon alpha/beta receptor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A45283; 148423; 148424; 148425; 148426; 148427; 148428; 148429
R;Uze, G; Lutfalla, G; Bandu, M.T.; Proudhon, D.; Mogensen, K.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 47144778, 1992
A;Title: Bahavior of a cloned murine interferon alpha/beta receptor expressed in homos A;Reference number: A45283; MUID:92262522; PMID:1533935
                                                                                                                                                                                                                             -----KTTVENELPPPENIEVSVQNQNYVLKWD----YTYANMTFQV 259
                                                                                                                                                                                                                                                                                                               QYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTS 122
                                                                                                                                                                                                                                                                                                                                                                                            ----LYKWKQIPDCENVKTTQCVFPQ 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAPN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 LPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAE 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 PKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVFQ-KGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 127-224 <RE2>
A;Cross-references: EMBL:U06238; NID:g497104; PIDN:AAC01749.1; PID:g755811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
X;Residues 243-254 «RE3>
A;Cross-references: EMBL:U06239; NID:9497106; PIDN:AAA65004.1; PID:9510261
A;Accession: 148426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: EMBL: U06241; NID: 9497110; PIDN: AAA65006.1; PID: 9755812
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NCBIP:102357)
                                                                         51;
        2; Length 557;
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A/Molecule type: mRNA
A/Residues: 1-590 < UZE>
A/Cross-references: GB:M89641; NID:g194111; PIDN:AAA37890.1;
A/Cross-references: GB:M89641; NID:g194111; PIDN:AAA37890.1;
A/Note: sequence extracted from NCBI backbone (NCBIN:102354, R;Lutfalla, G: Uze, G.
Gene 148, 343-346, 1994
A/Fitle: Structure of the murine interferon alpha/beta recept
9.5%; Score 136.5; DB 2;
nilarity 20.8%; Pred. No. 0.00039;
Conservative 39; Mismatches 115;
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A, Status: preliminary; translated from GB/EMBL/DDBJ
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Query Match
Best Local Similarity 22.2*
Matches 62; Conservative
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A; Residues: 1-489 <AGU>
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A;Residues: 1-292 <AND>
A;Cross-references: GB:M55390; NID:g165696; PIDN:AAA63469.1; PID:g165697
A;Cross-references: brain
B;Experimental source: brain
R;Pawashe, A: i Ezekowitz, M.; Lin, T.C.; Horton, R.; Bach, R.; Konigsberg, W.
A;Title: Maemost. 66, 315-320, 1991
A;Title: Molecular cloning, characterization and expression of cDNA for rabbit brain tis
A;Reference number: S23681; MUID:92081032; PMID:1746002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C, Keywords: blood coagulation, glycoprotein, lipoprotein, thiolegter bond, transmembrane F;1-12/Domain: signal sequence #status predicted <SIG> F;3-22/Product: tissue factor #status predicted <MIT> F;33-249/Domain: extracellular #status predicted <EXT> F;250-271/Domain: transmembrane #status predicted <TYM> F;272-292/Domain: intracellular #status predicted <IVM> F;41,114,154,167,182/Binding site: carbohydrate (Asn) (covalent) #status predicted F;79-69,216-239/Disulfide bonds: #status predicted Fs71-89,216-239/Disulfide bonds: #status predicted F;79-69,216-239/Disulfide Cys) (covalent) #status experimental
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A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 33-292 <PAM>
A,Cross-references: EMBL:X53521; NID:g1495, PIDN:CAA37597.1; PID:g3980170
C,Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
C;Comment: Expression of tissue factor can be induced in a variety of tissues by certain
C;Superfamily: tissue factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vibliance factor precursor - rabbit

NyAlternate names: coagulation factor III

Cispecias: Orycologus cuniculus (domestic rabbit)

Cispecias: Orycologus cuniculus (domestic rabbit)

Cipate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000

Cipate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000

Cipate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000

Cipate: 30-Sep-1993 #sequence Indoor 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 WGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QHTTTTKCEFSLLDTNVYIKTQPRVRAEEGNSTSSWNEVDPFIPFYTAHMSPPEVRLEAE 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIBA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: 148428
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Rossidues: 426-445 <RE6>
A;Cross-references: EMBL:U06242; NID:g497112; PIDN:AAA65007.1; PID:g755813
A;Accession: 14849: DNA
A;Ratus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: EMBL:U06244; NID:g497114; PIDN:AAA65008.1; PID:g510265
C;Genetics:
A;Gene: IFNAR
A;Introns: 177/3; 331/1
C;Keywords: cytokine receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 NIDVYIIDDNYTLKW-----SSHGESMG-----SVTFS-----AEYRTKDEAKWLKVPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 9.4%; Score 134.5; DB 2 Best Local Similarity 21.4%; Pred. No. 0.00063; Matches 45; Conservative 39; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTPHSSYCVVAEIYQPMLDRRSQRSEERCV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 LLPETTYCLEVKAIHPSLKKHSNYSTVQCI 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79
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receptor
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                                                                                                                                                                                                                                                                                                                                                                                                           130 PYYGRV-----RAASAGSYSE---WSMTPRFTPWWETKIDPPV------MNITQVN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 TYMARVLSYPARNGNTIGFPEEPPFRNSPEFTPYLDTNLGQPTIQSFEQVGTKLNVTVQD 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---RVFIINNSLEKEOKVYEGA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 ARTLVRRNGTFLSLRAVFGKDLN-----YTLYYWRASSTGKKTATTNTNEFLIDVDKGE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 YKIM----FSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 DLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVIL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 NISDHVGDPSNSLWYRVKARVGQKESAYAKSEEFAVCRDGKIGPPKLDIRKEEKQIMIDI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 23-Jul-1999
                                                                                                                                 11 LISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSC
                                                                                                                                                                                                                                                                                                                    21 LLGWLLAQVARAADT--TGRAYNLTWKSTNFKTILEWEP-----KSIDHV-YTVQIST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GB: J03143; NID: 9184650; PIDN: AAAS2731.1; PID: 9306915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RiAguet, M.; Dembio, Z.; Merlin, G.
Cell 5: 273-280; 1988
A;Title: Molecular cloning and expression of the human interferon-gamma
A;Reference number: A31555; MUID:89003065; PMID:2971451
                                                                89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71,
   Length 292;
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                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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9.3%; Score 132.5; DB 1;
22.2%; Pred. No. 0.00039;
ive 39; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

8.6%; Score 122.5; DB 2;
Best Local Similarity 20.1%; Pred. No. 0.0057;
Matches 56; Conservative 49; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 LAIPVSSL--NSQYCVSAEGVLHVWGVTTEKSKEVCITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Map position: 6q23-6q24
C,Superfamily: interferon gamma receptor
C,Keywords: cytokine receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 GSLLVILHAPNLPYR--YOKEKNVSIEDYYELLY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interferon gamma receptor precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Gene: GDB:IFNGR1; IFNGR
A,Cross-references: GDB:120688; OMIM:107470
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11;

Length 332;

DB 2;

66

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A)Residues: 11-32 cHEM>
A)Residues: 11-32 cHEM>
A)CTOSS-TEFETENCES: GB.869336; NID:9545841; PIDN:AAB30165.1; PID:9545842
A)CTOSS-TEFETENCES: GB.869336; NID:9545841; PIDN:AAB30165.1; PID:9545842
A)Actos mental source: early B-cell line Y16
A)NOte: sequence extracted from NCBI backbone (NCBIN:145654, NCBIP:145656)
C)Reywords: cytokine receptor
                                                                                                                                                                                                                                                                                                                        10 FLISFFLTGVAGTQSTHESLK----PQRVQFQSRNFHNILQWQPGRALTG-NSSVYFVQY
                                                                                                                                                                                                7.7%; Score 110.5; DB
20.2%; Pred. No. 0.04;
ive 33; Mismatches
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                                                                                                                                                                                                                            Similarity 20.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKPYRVYCLQTE 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTPHSSYCVVAE 242
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Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-515 < RES>
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                                                                                                                                                                                                                                                            51,
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                                                                                                                                                                                                      Query Match
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Matches 5
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Krewss Krews Andreace Caegulation feator III NALetrate names caegulation feator III NALetrate names caegulation feator III Species: Mus musculus (house mouse)
C,Date: 30-Sep-1933 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
C,Accession: AJ2118; AJ394m; AS per 1900 #text_change 22-Jun-1999
C,Accession: AJ2118; AJ394m; AS per 1900 #text_change 22-Jun-1999
R;Hartzell, S.; Ryder, K.; Lanahan, A.; Lau, L.F.; Nathans, D.
N;Hartzell, S.; Ryder, K.; Lanahan, A.; Lau, L.F.; Nathans, D.
N;Hartzell, S.; Ryder, K.; Lanahan, A.; Lau, L.F.; Nathans, D.
N;Hartzell, S.; Ryder, M.;
N;Hargentere number: AJ2118; MUID:89343974; PMID:2761539
A;Refeatore number: AJ2118; MUID:89343974; PMID:2761539
A;Refeatore number: AJ2118
A;Refeatore number: ABA
A;Refeatore number: ABA
A;Refeatore number: ABA
A;Refeatore number: AJ3046; MUID:91093171; PMID:1985911
A;Refeatore number: AJ5046; MUID:91093171; PMID:1985911
A;Refeatore number: AJ5046; MUID:91093171; PMID:1985911
A;Refeatore number: AJ5046; MUID:91093171; PMID:9109377
A;Note: 26-Thr was also found
C;Comment: Expression of tissue factor and integral membrane glycoprotein; thiolester bond; transmembrane factor C;Comment: Expression of tissue factor and number: Alamanian sequence factor and number: Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A49947
interferon gamma receptor beta subunit - mouse
interferon gamma receptor beta subunit - mouse
A49947
interferon gamma receptor beta subunit - mouse
C;Alterian annes: IPN-gamma R beta chain; IFN-gamma R species-specific cofactor; type
C;Accession: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A49947
R;Hemmi, S.; Bohni, R.; Stark, G.; Di Marco, F.; Aguet, M.
R;Hemmi, S.; Bohni, R.; Stark, G.; Di Marco, F.; Aguet, M.
A;Title: A novel member of the interferon receptor family complements functionality of A;Reference number: A49947; MUID:94170381; PMID:8124717
A;Accession: A49947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIQEPYYGRVRAASA------164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 FLGCLL-LQVTAGAGIPE-----KAFNLTWISTDFKTILEWQP----KPTNYTYTVQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 FLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.5%; Score 122; DB 1; Length 294; 22.7%; Pred. No. 0.0033; tive 36; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 NEFSIDVE---EGVSYCFFVQAMIFSRKTNQNSPGSSTVCTE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 AHRAVEIEALTPHSSYC--VVAEIYOPMLDRRSORSEERCVE 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64; Conservative
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Interferon alpha-beta receptor, beta subunit long form - human Cispecies: Homo sapiens (man)
Cipate: 24-May-1996 #sequence_revision 24-May-1996 #text_change 01-Dec-2000
CiAccession: 139073; 859502
R;Domanski, P.; Witte, M.; Kellum, M.; Rubinstein, M.; Hackett, R.; Pitha, P.; Colamon A; Biol. Chem. 270, 21866-21611, 1995
A;Title: Cloning and expression of a long form of the beta subunit of the interferon a A;Reference number: 139073; MUID:95394915; PMID:7665574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Cross-references: EMBL:U29584; NID:993040; PIDN:AACS0202.1; PID:9993041
R; Lutfalla, G; Holland, S.J.; Cinato, E.; Monneron, D.; Reboul, J.; Rogers, N.C.; Smi EMBO J. 14, 5100-5108, 1995
EMBO J. 14, 5100-5108, 1995
A; Title: Mutant U5A cells are complemented by an interferon-alpha-beta receptor subuni A; Reference number: S59501; MUID:96067138; PMID:7588638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; nucleic acid sequence not shown; not compared with conceptual t
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                                                                                                         65 KIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT--S 122
                                                                                                                                                                                                                                                                      123 ETSDIQEPY--YGRVRAASAGSYSEWSMTPRFTPWWETKIDPPV-MNITQVNGSLLV--- 176
                                                                                                                                                                                                                                                                                                                                                       96 RLKLFPHPFTVFLRVRÅKRGNLTSKWVGLEPFQHYENVTVGPPKNISVTPGKGSLVIHFS 155
                                                                                                                                                                                                                                                                                                                                                                                                                                       ----ILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHR--AVEIBA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----KSETQQEQVEGPFKSNSIVLGN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --PEDLKVVKNCANTTRSFCDLTDEWRSTHEAYV-TVLEGFSGNTTLFSCSHNFWLAIDM 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :| : : : | : | : | : | 133 SFEPPEFEIVGFTWHINVVVKFPSIVEEELQFDLSLVIEEGSEGIVK-----KHKPEIK 186
                         99
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                                                                                                                                                                                      -----EPNCTDITETKCDLTGG 95
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159 KIDPPVMNITQVNGSLLVILHAPNL-PYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQK
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C;Keywords: alternative splicing; cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43;
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.larity 20.3%; Pred. No. 0.29;
Conservative 39; Mismatches 99;
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                                                                                                                                                                                          67 SFI -----DGSWHRLL----
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interferon alpha/beta receptor precursor - human C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 09-Sep-1994 #text_change 05-Nov-1999 C; Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Nov-1999 C; Date: 05-Nov-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.1%; Score 101.5; DB 2; Length 331; Best Local Similarity 20.3%; Pred. No. 0.25; Matches 46; Conservative 39; Mismatches 99; Indels 43.
218 VYEGAHRAVEIBALTPHSSYCVVAEIYQPMLDRRSQ-RSEERCVEIP 263
                                                               187 GNWSGNFTYIIDKLIPNTNYCV--SVYLEHSDEQAVIKSPLKCTLLP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 VYEGAHRAVEJEALTPHSSYCVVAEIYOPMLDRRSQ-RSEERCVEIP 263
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OM protein - protein search, using sw model

December 12, 2003, 12:16:38 ; Search time 16.939 Seconds (without alignments) 730.151 Million cell updates/sec Run on:

Title: Perfect score:

US-10-047-264A-4 1432 1 MMPKHCFLGFLISFFLTGVA......XQPMLDRRSQRSEERCVEIP 263 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2	Description		พนธก	P13726 homo sapien	Q04790 bos t	Q61190 mus m	Q13651 homo	Q08334 homo	P30931 bos t	cavie		ovis		P24055 oryctolagus	P42533		P15260	Q95207 ovis	Q95141 bos t	P48551 homo	Р38484 hото	P08491 ross		Q8pim1 xanth		095116	•	_		P32226	Q8cvi4	P09986 escherichia	ex 1	Q05002 h replicase	
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ALIGNMENTS

MOUSE STANDARD; PRT; 575 AA. 110R MOUSE STANDARD; PRT; 575 AA. 110R-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1998 (Rel. 40, Last annotation update) 110-OCT-2001 (Rel. 40, Last annotation update) 1110-RAPA OR ILIOR. 11110.RAPA OR ILIOR. 11110.RAPA OR ILIOR.	Musumalia; Mouse, Mammalia; Mouse, Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCEI_TaxID=10090; [1] SEQUENCE FROM N.A. STRAIN=57BL/6 X AJ F1; TISSUE=Hematopoietic; MEDLINE=3406885; Pubmed=8248239; MEDLINE=3406885; Pubmed=8248239; "A receptor for interleukin 10 is related to interferon receptors."; "A receptor for interleukin 10 is related to interferon receptors."; Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993)!- FUNCTION: RECEPTOR FOR IL-10; BILNOS IL-10 WITH A HIGH AFFINITY!- SUBCELLULAR LOCATION: Type I membrane protein!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.	Ca Str Charri	### ### ##############################	122 N-LINKED (GLCNAC) (238 N-LINKED (GLCNAC) (64248 MW, 820B9CD576F686B7 CRC64
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RESULT.1 110R_MOUSE STANI 110	Mus muscutts (wouse) Bukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090; [1] SEQUENCE FROM N.A. STRAIN=C57BL/6 X AJ MEDINE=9468585; PH ME A.SY., Liu Y., "A receptor for inte Proc. Natl. Acad. SCIIII Y., "A receptor for inte Proc. Natl. Acad. SCIIII Y., "A subschilling RECEPTOR SUBSCENTION: RECEPTOR SUBSCENTION: RECEPTOR SUBSCENTION: RECEPTOR SUBSCENTION: BELKALLING SUBSCENTIO	This SWISS-PR between the the European use by non- modified and entities requ	EWEL, 112120; AAA16156. PIR, A49667; A49667. MGD; MGI:96538; 1110ra. InterPro; IPR000282; Cy Receptor; Transmembrane SIGNAL 17 241 TRANSMEM 242 262 DOWAIN 263 575 DISULFID 204 225 CARBOHYD 50 50 CARBOHYD 50 50 CARBOHYD 66 66	CARBOHYD CARBOHYD SEQUENCE
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16; Indels 77; Gaps Query Match
11.5%; Score 164.5; DB 1; Length 575;
Best Local Similarity 26.7%; Pred. No. 1.4e-07;
Matches 74; Conservative 37; Mismatches 89; Indels 77;

7 FLGPLISPPLTGVA-GTQSTHESLKPQRVQFQSRNPHNILOWQPGRALTGNSSVYFVQVK 65

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Rajkumar
  66 IMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETS 125
                                                               126 DIQEPYYG---RVRAASAGSYSEWSMT-PRFTPWWETKIDPPVMNITQV-----NGSLLV 176
                                                                               177 ILHAPNLPYRYQKEKNVSIEDYYELLY---RVFIINNSLEKEQKVYEGAHRAVEIBALT- 232
                                                                                                                       -----ALKQYGNSTWNDIHICRKAQALSCDLTTFTL 90
8 FLVTISSLSLEFIAYGT----ELPSPSYVWFEARFFQHILHWKP--IPNQSESTY---YE 58
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receptor for the initiation of the coagulation protease cascade.";
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                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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15-SEP-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                     ----PHSSYCVVAEIYQPMLDRR----SQRSEERCVEI 262
                                                                                                                                                                   295 AA.
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location of the factor VIIa binding site.";
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factor refined to 1.7-A resolution.";
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Submitted (JUL-2000)
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                                                                                              DATABASE: NAME=PROW; NOTE=CD guide CD142 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd142.htm".
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GO; GO:001801; F:blood coagulation factor activity; TAS.
InterPro; IPR000189; Cyrok receptor 2.
InterPro; IPR001189; Tissue factor.
Pfam; PF01108; Tissue fac; I.
PRINTS; RR00346; TISSUERACTOR.
Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein; Palmitate; 3D-structure; Polymorphism.
CAN ALSO BE INDUCED BY THE INFLAMMATORY MEDIATORS INTERLEUKIN AND TWF; AS WELL AS BY ENDOTOXIN, TO APPEAR ON MONOCYTES AND VASCULAR ENDOTHELIAL CELLS AS A COMPONENT OF CELLULAR IMMUNE RESPONSE.
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                                                                              SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.
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EMBL; A19048; CAA01438.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 PYYGRV-----RAASAGSYSE--WSMTPRFTPWWETKI-DPPVMNITQVNGSLLVILHA 180
                                                                                                                                                                                                                                                                                                                                                71 SMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSE-TSDIQE 129
                                                                                                                                                                                                                                                                                                                                                                                 102 TYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPTIQSFEQVGTKVNVTVED 161
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                                                                                                                                                                                                                 11 LISFFLIGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSC 70
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Lim J.-K., Langer J.A.;
Lin J.-K., Langer J.A.;
Lin J.-K., Langer J.A.;
Lin J. Lin
                                                                                                                                                                                                                                                                          21 LLGWVFAQVAGASGTTNTVAAYNLTWKSTNFKTILEWEPKPV----NQVYTVQ-----I
                                                                                                                                                     Gaps
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01-NOV-1997 (Rel. 35, Last annotation update)
Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC)
IFNARI OR IFNAR.
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Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Butheria, Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinee; Bos
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                                                                                      11.4%; Score 163; DB 1; Length 295; 23.4%; Pred. No. 8.2e-08; ive 45; Mismatches 100; Indels 58;
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                                                                                                                                                  62; Conservative
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Best Local Similarity
Matches 62; Conserv
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Q04790;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 SYSEWSMTPRFTPWWETKIDPPVMNITQV-NGSLLVILHAPNLPYRYQKEKNVSIEDYYB 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42; Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                        INTERFERON-ALPHA/BETA RECEPTOR ALPHA
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Interleukin-10 receptor beta chain precursor (IL-10R-B) (IL-10R2)
(Cytokine receptor class-II CRF2-4).
                                                                                                                                                                                                                                                                                  (POTENTIAL).
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MEDLINE=97199375; PubMed=9047351;
Gibbs V.C., Pennica D.;
"CRP2-1 isolation of cDNA clones encoding the human and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 560,
                                                                                                                                                                                                                                                                                                                                                                                                                                                11.0%; Score 158; DB 1; Length 560
24.1%; Pred. No. 5.3e-07;
ive 38; Mismatches 100; Indels
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                                                                                                                                                                        EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL)
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                                                                                                      Receptor; Transmembrane; Glycoprotein; Signal.
SIGNAL 1 24 BY SIMILARITY.
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        PIR; S27387; S27387.
InterPro; IPR000282; Cytok receptor_2.
InterPro; IPR0013861; FN III.
InterPro; IPR001187; Tissue factor.
Pfam; PF01108; Tissue fac; I.
SWART; SM00060; FN3; Z.
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CHARACTERIZATION,
MEDLINE=98130620; PubMed=9463407;
                                                                                                                                                                                                                                                                                                                                                                                                                     63818 MW;
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Q61190;
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Spencer S.D., Di Marco F., Hooley J., Pitts-Meek S., Bauer M., Ryan A.M., Sordat B., Gibbs V.C., Aguet M.;

Ryan A.M., Sordat B., Gibbs V.C., Aguet M.;

10 receptor.";

J. Exp. Med. 197:571-578 (1998).

-1- FUNCTION: RECEPTOR FOR IL-10 AND IL-22. SERVES AS AN ACCESSORY

CHAIN ESSENTIAL FOR THE ACTIVE IL-10 RECEPTOR COMPLEX AND TO

INTIALE IL-10-INDUCED SIGNAL TRANSDUCTION EVENTS.

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- SUMLIARITY: Concains 2 fibronectin type III domains.

-1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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. . .) (POTENTIAL).
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CYTOPLANIC (POTENTIAL).
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(Rel. 36, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Mar
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  :| : | : | : | : | 138 FILGKIQLP-----RPKMAPANDTYESIFSHFREYEIAIRKVPGNFTFTHKKVKHENF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93300510; PubMed=8314576;
Lutfalla G., Gardiner K., Uze G.;
Lutfalla G., Gardiner K., Uze G.;
A new member of the cytokine receptor gene family maps on chromosome 2.1 at less than 35 kb from IFNAR.";
Genomics 16:366-373 (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20469498; PubMed=10875937; Xie M.-H., Aggarwal S., Ho W.-H., Foster J., Zhang Z., Stinson J., Xie M.-H., Aggarwal S., Ho W.-H., Foster J., Zhang Z., Stinson J., Wood W. T., Goddard A.D., Gurney A.L.; Britchlekin (IL)-22, a novel human cytokine that signals through the interferon receptor-related proteins CRF2-4 and IL-22R."; J. Biol. Chem. 275:31335-3139(2000).

-I. FUNCTION: RECEPTOR FOR IL-10 AND IL-22. SERVES AS AN ACCESSORY CHAIN ESSENTIAL FOR THE ACTIVE IL-10 RECEPTOR COMPLEX AND TO INTIATE IL-10-INDUCED SIGNAL TRANSDUCTION EVENTS.

-I. SUBCELLULAR LOCATION: Type I membrane protein.

-I. SIMILARITY: Contains 2 fibronectin type III domains.

-I. SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pestka S.; "Identification and functional characterization of a second chain of
                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last sequence update)
11ce-FEB-2003 (Rel. 41, Last annotation update)
11nterleukin-10 receptor beta chain precursor (IL-10R-B) (IL-10R2)
1Cytokine receptor class-II CRF2-4).
1L10RB OR CRFB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=96054036; PubMed=7563119;
Lutfalla G., McInnis M.G., Antonarakis S.E., Uze G.;
"Structure of the human CRFB4 gene: comparison with its IFNAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kotenko S.V., Krause C.D., Izotova L.S., Pollack B.P., Wu W.,
                                                                                   232 TPHSS----YCVVAEIYQPMLDRRSQR---SEERCVEI 262
                                                                                                                       191 SLLTSGEVGEFCVOV---KPSVASRSNKGMWSKEECISL 226
                                                                                                                                                                                                                                                                                     325 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the interleukin-10 receptor complex.";
EMBO J. 16:5894-5903(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97459974; PubMed=9312047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Mol. Evol. 41:338-344(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z17227; CAA78933.1; -. EMBL; U08988; AAA86872.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A47003; A47003.
HSSP; P13726; 1TFH.
Genew; HGNC:5965; IL10RB.
                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION.
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NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                     HUMAN
                                                                                                                                                                                                                                                                                                       008334:
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I10S_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSETSDI--QEPYYGRVRAASAGSYSEWSMT-PRFTPWWETKIDPPVMNITQV-----NG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 TAVTLDLYHSNGYRARVRAVDGSRHSNWTVTNTRFS-----VDEVTLTVGSVNLEIHNG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVF-IINNSLEKEQKVYEGAHRAVEIEAL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                              MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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15-SEP-2003 (Rel. 42, Last annotation update)
Interleukin-10 receptor alpha chain precursor (IL-10R-A) (IL-10R1)
IL10RA OR IL10R.
                                               Homo sapiens (Human),
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERLEUKIN-10 RECEPTOR ALPHA CHAIN.
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GO; GO:0004920; F:interleukin-10 receptor activity; TAS.
GO; GO:0004872; F:receptor activity; TAS.
InterPro; IPR000282; Cytok receptor 2.
Seceptor; Transmembrane; GlycoproteIn; Signal; 3D-structure.
SIGNAL
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; Pred. No. 1e-06;
42; Mismatches 103; Indels 7
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(GLCNAC. . .)
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22.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 EWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQ--KEKNVSIEDYYELL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 DW-VNITFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKIENEYETWTMKOV----YNSWT 153
                                                                                                                                                                                                                                                                                                                                                                                                                   31 PORVQFQSRNFHNILQWQPGRALTGN--SSVYFVQYKIMFSCSMKSSHQKPSGCWQHISC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                         24 PENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIF------62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------YGDHTLRVRAEFADEHS 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYOPMLDRRSQRSEERC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 YNVQYWKNGTDEKFQITPQYDFEV-LRNLEPWTTYCVQVRGFLPDRNKAGEWSEPVC 209
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea;
Bovidae, Bovinae, Bos.
                                                                                                                                                               POTENTIAL.
INTERLEUKIN-10 RECEPTOR BETA CHAIN.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                  . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                             59;
                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 325;
      GO; GO: 0016621; C: integral to membrane; TAS.
GO; GO: 00016621; C: plasma membrane; TAS.
GO; GO: 0004820; F: interleukin.-10 receptor activity; TAS.
GO; GO: 0004872; F: receptor activity; TAS.
GO; GO: 0006955; F: receptor activity; TAS.
GO; GO: 0006954; P: inflammatory response; TAS.
GO; GO: 0007165; P: inflammatory response; TAS.
GO; GO: 0007165; P: inflammatory response; TAS.
InterPro; IPR003961; FN III.
InterPro; IPR003961; FN III.
InterPro; IPR001981; Tissue factor.
Pfam; PF01108; Tissue factor.
SWART; SM00060; FN3; Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Adrenal gland;
MEDLINE=92109720; PubMed=1764065;
Makayenoki Y., Muta T., Miyata T., Iwanaga S.;
"CDNA and amino acid sequences of bovine tissue factor.";
Biochem. Biophys. Res. Commun. 181:1145-1150(1991).
                                                                                                                                                                                                                                                                                                                                                                                            89; Indels
                                                                                                                                                                                                                                                                                                        A -> D (IN REF. 2).
FLGHP -> VGRME (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                             66706C79F8514B23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-CT-201 (Rel. 40, Last annotation update)
Tissue factor precursor (TF) (Coagulation factor III).
                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . . ) (
                                                                                                                                                                                                                                                                                                                                                                   10.4%; Score 149.5; DB 1
24.1%; Pred. No. 1.7e-06;
iive 32; Mismatches 89
                                                                                                                                                   Receptor; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                  MISSING (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                              37011 MW;
                                                                                                                                                                                                                                                                                                                                                                                          57; Conservative
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                                                                                                                                                                                                                                                                                                                                            325 AA;
                                                                                                                                                                                                                                                                                                                                                                               Similarity
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CONFLICT
CONFLICT
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SEQUENCE
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P30931;
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                                                                                                                                                                                                                                    DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 SMKSSHOKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSE-TSDIQE 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 PYYGRVRAASAGSYSE----WSMTPRFTPWWETKI-DPPVMNITQVNGSLLVILHAPNL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 LVR-ANSAFLSLRDVFGKDLNYTLYYWKASSTGKKKATTNTNGFLIDVD---KGENYCFH 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSC 70
                                                                                           ROLE IN
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InterPro; IPR000282; Cytok receptor_2.
InterPro; IPR001282; Tissue_factor.
Pfam; PF01108; Tissue_fac; I.
PRINTS; PR00346; TISSUEFACTOR.
PROSTITE; PS00621; TISSUE FACTOR; 1.
Glycoprofein; Blood coagulation; Transmembrane; Signal; Lipoprotein; Palmitate.
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                                           CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES FACTORS IX OR X BY SPECIFIC LIMITED PROTOLYSIS. TF PLAYS A ROLE NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND PROPAGATION OF THE COMULATION PROTEASE CASCADE. SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.
FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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9.74; Scote 2007;

Best Local Similarity 22.64; Pred. No. 1.6e-05;

Matches 59; Conservative 43; Mismatches 104; Indels
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5E471D92BFBCE163 CRC64;
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EXTRACELLULAR (POTENTIAL)
POTENTIAL.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tissue factor precursor (TF) (Coagulation factor III).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | | ::::| | :|
VQAVILSRRVNQKSPESPIKC 238
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RESULT 9
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                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 SMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKBDCWGTQELSCDLTSETS-DIQE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 PYYGRVRAA---SAGSYSE--WSMTPRFTPWWETKIDPP------VMNIT----- 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shi R.J., Li W.Z., Marder V.J., Sporn L.A.;

"Cloning of guinea pig tissue factor cDNA: comparison of primary
"Cloning of guinea pig tissue factor cDNA: comparison of primary
structure among six mammalian species.";

Thromb. Haemost. 83:455-461(2000).

-!- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
CIRCULATING PACTOR VII OR VIIA. THE [TP:VIIA] COMPLEX ACTIVATES
FATORS IX OR X BY SPECIFIC LIMITED PROTOLYSIS. TF PLAYS A ROLE IN
NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 LIGWVLVQVAGAEGI--PVKPYNLTWKSTNFKTILEWEPKPI----NNVYTVQ----IST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Signal; Lipoprotein;
                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WKS MOTIF.

N.LINKED (GLCNAC. . .) (POTENTIAL)

N.LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67;
P3.
Cavia porcellus (Guinea pig).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostc
Mammalia, Butheria, Rodentia, Hystricognathi, Caviidae, Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.5%; Score 136.5; DB 1; Length 289; 24.9%; Pred. No. 2.4e-05; ive 32; Mismatches 52; Indels 67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILMARTY.
BY SIMILMARTY.
PALMITATE (BY SIMILMARTY).
MW; 7AB97F8F58199FB1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY
                                                                                                                                                                                                                                                                                                                                  HSSP; P13726; ITFH.
InterPro; IPR000282; Cytok_receptor_2.
InterPro; IPR001187; Tissue_factor.
Pfam; PF01108; Tissue_fac; I.
PRINTS; PR00346; TISSUEPACTOR.
PROSITE, PS00621; TISSUE FACTOR; PACSTER.
PROSITE; PS00621; TISSUE FACTOR; FALSE NE
                                                                          TISSUE=Lung;
MEDLINE=20206020; PubMed=10744153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- OVNGSLLVI -- LHAPNLPY 185
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                                                                                                                                                                                                                                                                                                                             EMBL; AF131949; AAF36523.1; -.
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hes 50; Conservative
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289 AA;
                                                                 SEQUENCE FROM N.A.
                                           NCBI_TaxID=10141;
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248
269
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GO; GO:0005887; C:integral to plasma membrane; TAS.

GO; GO:0004905; F:interferon-alpha/beta receptor activity; TAS.

GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.

GO; GO:0007559; P:response to viruses; TAS.

GO; GO:000815; P:response to viruses; TAS.

InterPro; IPR003615; P:II.

SMART; SM00060; FN3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95059042; PubMed=7526154; Colamonici O., Yan H., Domanski P., Handa R., Smalley D., Mullersman J., Witte M., Krishnan K., Krolewski J.; Mullersman J., Witte M., Krishnan K., Krolewski J.; Direct binding to and tyrosine phosphorylation of the alpha subunit of the type I interferon receptor by p135tyk2 tyrosine kinase."; Mol. Cell. Biol. 14:8133-8142(1994).

-!- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS INCLUDING JAKS, TYKZ, STAT PROTEINS AND IFN-R ALPHA-AND BETA-SUBUNITS THEMSELVES.
                                                               01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC).
IFNARI OR IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUB SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND EVEN ON THE SURPACE OF MOST IFN-RESISTANT CELLS.
-!- FURN ON THE SURPACE OF MOST IN-RESISTANT CELLS.
-!- PITM: PHOSPHORYLATED ON TYROSINE REDUGS BY TYKZ TROSINE KINASE.
-!- SIMILARITY: CONTAINS 2 fibronectin type III domains.
-!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-92129376; PubMed-1370833;
Luffalla G., Gardiner K., Proudhon D., Vielh B., Uze G.;
Lufte atructure of the human interferon alpha/beta receptor gene.";
J. Biol. Chem. 267:2802-2809(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=90124632; PubMed=2153461;
Uze G., Lutfalla G., Gresser I.;
"Genetic transfer of a functional human interferon alpha receptor into mouse cells: cloning and expression of its CDNA.";
cell 60:225-234(1990).
                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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557 AA
PRT;
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EMBL; X60459; CAA42992.1; -.
PIR; A32694; A32694.
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557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAPN 182
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC)
(Interferon alpha/beta receptor-1).
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Endometrium,
MEDLINE=97135690; PubMed=8981227;
Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.;
"Structure of an ovine interferon receptor and its expression in
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PHOSPHORYLATION (BY TYK2)
N-LINKED (GLCNAC. . .) (PO
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G -> A (IN REF. 2).
0F6744C8AlADBE73 CRC64;
EXTRACELLULAR (POTENTIAL)
               POTENTIAL.

CYTOPLASMIC (POTENTIAL)

BY SIMILARITY.

BY SIMILARITY.
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20.8%; Pred. No. 5.3e-05;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                 pregnancy.";
Endocrinology 138:4757-4767(1997).
Endocrinology 138:4757-4767(1997).
-!- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYF
-!- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND STALGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS INCLUDING JAKS, TYKZ, STAT PROTEINS AND IFN-R ALPHA-AND BETA-SUBUNITS THEMSELVES.
                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUB SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT
CONCEPTUS AT DAY 15 OF PREGNANCY.
-!- SIMILARITY: CONTAINS 2 fibronectin type III domains.
-!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE PAMILY OF RECEPTORS.
TISSUE=Endometrium;
MEDLINE=98006426; PubMed=9348203;
Mathialagan N., Klemann S.W., Roberts R.M.;
Han C.-S., Mathialagan N., Klemann S.W., Roberts T.M.;
"Molecular cloning of ovine and bovine type I interferon receptor subunits from uteri, and endometrial expression of messenger ribonucleic acid for ovine receptors during the estrous cycle and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERFERON-ALPHA/BETA RECEPTOR ALPHA
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CYTOPLARING (POTENTIAL).
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N-LINKED (GLCNAC. ..) (POT
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Interpro; IPR003961; FN_III
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197 DYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAE--IYQPMLDRRSQR 254
                            364 OLÝPLVYEVIFWENTSNAERKVLE-KRIDFIFPNLKPLTVÝCVKARALIENDRWNKGSSY 422
                                                                                                                                                                                                                                                                                                                                                                                  Uze G., Lutfalla G., Bandu M.T., Proudhon D., Mogensen K.E.;
"Behavior of a cloned murine interferon alpha/beta receptor expressed
in homospecific or heterospecific background.";
Proc. Natl. Acad. Sci. U.S.A. 89:4774-4778 (1992)
- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
INCLUDING JAKS, TYRZ, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
                                                                                                                                                                                           01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC)
IFNARI OR IFNAR OR IFAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: Contains 2 fibronectin type III domains.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERFERON-ALPHA/BETA RECEPTOR ALPHA
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7EC6DFF370185D3A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC.)

N-LINKED (GLCNAC.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor; Transmembrane; Glycoprotein; Signal.
SIGNAL 1 26 POTENTIAL.
                                                                                                                                                                   590 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000282; Cytok receptor_2.
InterPro; IPR003961; FN_III.
SMART: SM00060; FN3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN.
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=92262522; PubMed=1533935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65776 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M89641; AAA37890.1; -.
                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A45283; A45283.
MGD; MGI:107658; Ifnar1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNITS THEMSELVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43
109
181
214
                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00060; FN3
                                                         255 SEERC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                590 AA;
                                                                                        423 SDTVC 427
                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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450
78
                                                                                                                                                              INR1 MOUSE
P33896;
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TRANSMEM
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SEQUENCE
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7;

Gaps

27;

45; Conservative

Matches

Local Similarity

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    NSSVYFV--QYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKY---GQRQWKNKEDC 110
                                                                                                                                                           111 WGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQV 170
                                                                                                                                                                                                                                  QHTTTTKCEFSLLDTNVYIKTQFRVRAEEGNSTSSWNEVDPFIPFYTAHMSPPEVRLEAE 138
                                                                                                                                                                                                                                                                                                                                                                                                      139 DKAILVHISPPG-----QDGNMWALEKPSFSYTIRIWQKS-SSDKKTINSTYYVEKIPE 191
                                                                               78
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STRAIN=New Zealand white; TISSUE=Brain;
MEDLINE=92081012; Pubmed=1746002;
Pawashe A., Ezekowitz M., Lin T.C., Horton R., Bach R., Konigsberg W.;
"Molecular cloning, characterization and expression of cDNA for rabbit brain tissue factor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH CITCULATING PACTOR VII OR VIIA. THE [TF-VIIA] COMPLEX ACTIVATES PACTORS IX OR X BY SPECIFIC LIMITED PROTOXSIS. TF PLAYS A ROLE IN NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
                                                          34 NIDVYIIDDNYTLKW-----SSHGESMG-----SVTFS-----AEYRTKDEAKWLKVPEC
                                                                                                                                                                                                                                                                                                                      171 NGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91200676; PubMed=1840552;
Andrews B.S., Rehemtulla A., Fowler B.J., Edgington T.S., Mackman N.;
"Conservation of tissue factor primary sequence among three mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98266351; PubMed-9605315; Muller Y.A., Kelley R.F., de Vos A.M.; "Hinge bending within the cytokine receptor superfamily revealed by the 2.4 A crystal structure of the extracellular domain of rabbit Protein Sci. 7:1106-1115(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01.MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tissue factor precursor (TF) (Coagulation factor III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROPAGATION OF THE COAGULATION PROTEASE CASCADE. SUBCELLULAR LOCATION: TYPE I membrane protein. TISSUE SPECIFICITY: BRAIN, HEART. SIMILARITY: BELONGS TO THE TISSUE PACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 36-240.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIPHSSYCVVAEIYOPMLDRRSQRSEERCV 260
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LLPETTYCLEVKAIHPSLKKHSNYSTVQCI 221
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P24055;
26
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    160 ARTLVRRNGTFLSLRAVFGKDLN-----YTLYYWRASSTGKKTATTTNTNEFLIDVDKGE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . Z
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HSSP; P13726; 1FAK.
InterPro; IPR001282; Cytok receptor_2.
InterPro; IPR001282; Cytok receptor_2.
InterPro; IPR001187; Tissue factor.
Pfam; PF01108; Tissue fac; 1.
PRINTS; PR00346; TISSUEFACTOR.
PROSITE; PS00621; TISSUE FACTOR; 1.
Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein; GIGNAL.
1 28 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tissue factor precursor (TF) (Coagulation factor III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE FACTOR.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
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WKS MOTIF.
N-LINKED (GLCNAC. . . ) (P. N-LINKED (GLCNAC. . ) (P. N-LINKED (GLCNAC. . . ) 
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EE4C15B4E3628D48 CRC64;
                                                                HRAVEIEALTPHSSYCVVAEIYOPMLDRRSQRSEERCVE
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                                                                                                                                                                                                       295
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295
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DISULPID
LIPID
SEQUENCE
                                                                  223
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 TYMARVLSYPARNGNTTGFPEEPPFRNSPEFTPYLDTNLGQPTIQSFEQVGTKLNVTVQD 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 PYYGRV-----RAASAGSYSE---WSMTPRFTPWWETKIDPPV-------MNITQVN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSLLVILHAPNLPYR--YQKEKNVSIEDYYELLY-----RVFIINNSLEKEQKVYEGA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 LISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 LIGHLLAQVARAADT--TGRAYNLTWKSTNFKTILEWEP------KSIDHV-YTVQIST 70
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EMBL; X53521; CAA37597.1; -.
PIR; JU0441; KFRB3.
PDB; 1A21; 27-MAY-98.
InterPro; 1PR0001287; Cytok_receptor_2.
InterPro; 1PR001187; Tissue_factor.
Pfam; PF01108; Tissue_fac; 1.
PRINTS; PR00346; TISSUE_RACTOR.
PROSTE; PS00621; TISSUE_RACTOR.
Glycoprotein; Blood coaqulation; Transmembrane; Signal; Lipoprotein; Palmitate; 3D-structure.
                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
WKS MOTIF.
WKS MOTIF.
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22.2%; Pred. No. 5.6e-05;
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InterPro; IPR001282; Cytok receptor_2.
InterPro; IPR001187; Tissue_factor.
Pfam; PF01108; Tissue_fac; 1.
PRINTS; PR00346; TISSUERACTOR.
PR051TE; PS00621; TISSUE FACTOR; 1.
Palmitate.

TISSUE FACTOR. EXTRACELLULAR (POTENTIAL).

DOMAIN TRANSMEM

DOMAIN

SIGNAL

POTENTIAL. CYTOPLASMIC (POTENTIAL).

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                                                                                                                                                                                                          125
                                                                                                                                                                                                                                                                                                                                                                                 172 GSLLVILHAPNLPYRYQKEKNVSIEDYYELLYR--VFIINNSLEKEQKYYEGAHR---AV 226
                                                                                                                                                                                                                                                                                                                                          126 DIQEPYYGRV------RAASAGSYSE---WSMTPRFTPWWETKIDPPVMNITGVN 171
                                                                          99
                                                                                                                                       64
                                                                                                                                                                                                                                                                       MEDLINE=89343974; PubMed=2761539;

MEDLINE=89343974; PubMed=2761539;

Hartzell S., Ryder K., Lanahan A., Lau L.F., Nathans D.;

Hartzell S., Ryder K., Lanahan A., Lau L.F., Nathans D.;

Hartzell S., Ryder K., Lanahan A., Lau L.F., Nathans D.;

Hartzell S., Ryder K., Lanahan Lissue factor.";

Mol. Cell. Biol. 9:2567-2573(1989).

-! FUNCTION: INTIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH

CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES

FACTORS IX OR X BY SPECIFIC LIMITED PROTOLYSIS. TF PLAYS A ROLE IN NORWAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND PROPAGATION PROTEASE CASCADE.

-! SUBCELLULAR LOCATION: Type I membrane protein.

-! SINILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.
                                                                       7 FLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKI
                                                                                                                                       17 FLGFLLLQVAVG-AGTPPG----KAFNLTWISTDFKTILEWQP----KPTNYTYTVQ---
                                                                                                                                                                                                   67 MFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSE-TS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning of murine tissue factor and regulation of gene expression by transforming growth factor type beta 1."; J. Biol. Chem. 266:496-501(1991).
       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-91093171; PubMed-1985911;
Ranganathan G., Blatti S.P., Subramaniam M., Fass D.N., Maihle N.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
       93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 EIEALTPHS-----SYCVVAE--IYOPMLDRRSQRSEERCVE 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 GRKINITHINEFLIDVEKGVSYCFFAQAVIFSRKINHKSPESITKCTE 244
       92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TF MOUSE STANDARD; PRT; 234 MA.
P20352;
01-FBE-1991 (Rel. 17, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tissue factor precursor (TF) (Coagulation factor III).
       Mismatches
37;
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EMBL; M26071; AAA40414.1; -.
PIR; A32318; KFMS3.
HSSP; P13726; 1FRX.
MGD; MGI:88381; F3.
   66; Conservative
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67 MFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSE-TS 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 ---MNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 GRKLNVVVKDSLTLVRKNGTFLTLRQVFGKDLG----YIITYRK---GSSTGKKTNITNT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 FLGCLLLQVIAG-AGIPE----KAFNLTWISTDFKTILEWQP----KPTNYTYTVQ--- 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 FLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKI
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                                                                                                                                                                                                                                                                                                                                                                        247 WKS MOTIF.
37 N-LINKED (GLCNAC. .) (POTENTIAL).
57 N-LINKED (GLCNAC. .) (POTENTIAL).
169 N-LINKED (GLCNAC. .) (POTENTIAL).
200 N-LINKED (GLCNAC. .) (POTENTIAL).
83 BY SIMILARITY.
241 BY SIMILARITY.
275 PALMIARITY.
276 I -> T (IN REF. 2).
286 MY, A306101293C31FA0 CRC64;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aguet M., Dembic Z., Merlin G.; "Molecular cloning and expression of the human interferon-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INGR HUMAN STANDARD; PRT; 489 AA.
P15560;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Interferon-gamma receptor alpha chain precursor (CDw119)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phillimore B.; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. [3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 AHRAVEIEALTPHSSYC--VVAEIYQPMLDRRSQRSEERCVE 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.7%; Score 124; DB 1; 22.7%; Pred. No. 0.00035;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 AA;
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Best Local Similarity
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489 AA;
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Usage by and for commercial
         TISSUE-Prosected.

X MEDINE-22388257; PubMed=12477932;

MEDINE-22388257; PubMed=12477932;

Strausberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hand N.K.,

Hopking R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Angleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S.W., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Nillalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Nillalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Blakesley R.W., Touchman J.W., Schentz J., Myers R.M.,

Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

In Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 26-248.
MEDLINE=95342235; PubMed=7617032;
Walter M.R., Windsor W.T., Nagabhushan T.L., Lundell D.J., Lunn C.A., Zauodny P.J., Narula S.K.;
Crystal structure of a complex between interferon-gamma and its soluble.high-affinity receptor.";
Nature 376:230-235(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98035727; PubMed=9367779; Sogabe S., Stuart F., Henke C., Bridges A., Williams G., Birch A., Sogabe S., Stuart F., Henke C., Bridges A., Williams G., Birch A., Winkler F.K., Robinson J.A.; Neutralizing epitopes on the extracellular interferon gamma receptor "Neutralizing epitopes on the extracellular interferon gamma receptor (IFNgammaR) alpha-chain characterized by homolog scanning mutagenesis and X-ray crystal structure of the A6 fab-IFNgammaR1-108 complex."; J. Mol. Biol. 273:882-897(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Monomer.

SUBURILAR LOCATION: Type I membrane protein.

PIW: PHOSPHORYLATED AT SER/THR RESIDUES.

SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

SIMILARITY: Contains 2 fibronectin type III domains.

SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.

DATABASE: NAME=PROW; NOTE=CD guide CDw119 entry;

WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw119.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF COMPLEX WITH ING.
MEDLINE=20444407; PubMed=10986460;
Thiel D.J., le Du M.-H., Walter R.L., D'Arcy A., Chene C.,
Thiel D.J., agrotta G., Winkler F.K., Ealick S.E.;
"Observation of an unexpected third receptor molecule in the crystal structure of human interferon-gamma receptor complex.";
Structure 8:927-936(2000).
-i- FUNCTION: RECEPTOR FOR INTERPERON GAMMA. TWO RECEPTORS BIND ONE INTERFERON-GAMMA DIMER.
                                                                                                                                                                                                                                                                                                                          MEDLINE=93183911; PubMed=8443182;
Stueber D., Friedlein A., Fountoulakis M., Lahm H.-W., Garotta G.
Aligument of disulfide bonds of the extracellular domain of the
interferon gamma receptor and investigation of their role in
biological activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 28-122 IN COMPLEX WITH
                                                                                                                                                                                                                                                                                                                   DISULFIDE BONDS, PARTIAL SEQUENCE, AND MUTAGENESIS.
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EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                               GO: GO:0005887; C:integral to plasma membrane; TAS.
GO: GO:0003800; F:antiviral response protein activity; TAS.
GO: GO:0004800; F:interferon-gamma receptor activity; TAS.
GO: GO:0006955; P:interferon-gamma receptor activity; TAS.
GO: GO:000619; P:response to pathogenic bacteria; TAS.
GO: GO:0005615; P:response to viruses; TAS.
GO: GO:0007615; P:response to viruses; TAS.
InterPro; IPR000282; Cytok receptor.
Receptor; Transmembrane; GlycoproteIn; Signal; Phosphorylation;
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CYTOPLASMIC (POTENTIAL)
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SIGNAL 17
Query Match 8.6
Best Local Similarity 20.1
Matches 56; Conservative
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GTQSTHESLKPQRV		SHQKPSGCWQHISCNFPGCRTLAKYC	50 YQIMPQVPVFTVEVKN	119 DLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVIL	86 NISDHVGDPSNSLWYRVKARVGQKESAYAKSEEFAVCRDGKIGPPKLDIRKEEKQIMIDI	SIEDYYELLYRVFIINNSLE	146 FHPSV-FVNGDEGEVDYDPETTCYIRVYNVYVRRNGSEIQYKILTQKEDDCDEIQCQ 201	224 RAVEIEALTPHSSYCVVAEIYOPMLDRRSORSEERCVEI 262	202 LAIPVSSLNSQYCVSAEGVLHVWGVTTEKSKEVCTTI 238
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Search completed: December 12, 2003, 12:26:06 Job time : 18.939 secs

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67 MFSCSMKSSHOKPSGCWQHISCNFPGCRTLAK 98
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APPLICANT: Fouser, Lynette
APPLICANT: Liu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-404-6
 US-10-047-264A-4
RESULT 2
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Sequence 28, Appli
Sequence 22, Appli
Sequence 42, Appli
Sequence 1340, Ap
Sequence 1345, Ap
Sequence 1345, Ap
Sequence 1942, Ap
Sequence 5085, Appli
Sequence 65, Appli
Sequence 65, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 18, Appli
Sequence 18, Appli
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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(cgnz_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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(cgnz_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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(cgnz_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
(cgnz_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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12 US-10-047-264A-4
12 US-10-0313-932-28
12 US-10-312-088-42
10 US-09-764-864-1340
10 US-09-764-864-1349
11 US-09-764-891-3345
12 US-10-094-749-1942
10 US-09-738-626-5085
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15 US-10-188-012-33
11 US-09-813-153-138
11 US-09-913-133-48
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1 MFSCSMKSSHQKPSGCWQHISCNFPGCRTLAK 32
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                                                                                                                                                                                                                         684280 seqs, 185983659 residues
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                                                                                                                                 US-10-047-264A-4_COPY_67_98
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Maximum Match 100%
Listing first 45 summaries
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                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence 28, Appl Sequence 21, Appl Sequence 24, Appl Sequence 4, Appl Sequence 5, Appl Sequence 50, Appl Sequence 6, Appl Sequence 6, Appl Sequence 18, Appl Sequence 34, App
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Sequence 34477, A
Sequence 49, Appl
Sequence 16, Appl
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Sequence 1662, App
Sequence 7, Appli
Sequence 10, Appl
Sequence 16, Appl
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| Bublication No. US20030022827A1
| Publication No. US20030022827A1
| GENERAL INFORMATION:
| APPLICANT: WEISS, BERTRAM
| APPLICANT: ASADULLAH, KHUSRU
| APPLICANT: ASADULLAH, CUUSELIA
| TITLE OF INVENTION: PAMILY CLASS 2
| FILE REFERENCE: SCH-1788
| CURRENT APPLICATION NUMBER: US/09/961,404
| CURRENT FILLING DATE: 2001.09-25
| NUMBER OF SEQ ID NOS: 19
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 6
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2 US-09-836-353A-48
2 US-10-354-047A-7
2 US-10-354-047A-18
2 US-10-354-047A-28
3 US-10-354-047A-28
5 US-10-072-602B-23
5 US-10-072-602B-24
5 US-10-072-602B-24
6 US-10-072-602B-24
7 US-09-764-903-50
7 US-09-764-903-50
7 US-09-986-552-6
2 US-10-024-18
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3 US-10-023-899-18
5 US-10-023-899-18
5 US-10-023-899-18
6 US-09-924-154-14
7 US-09-964-761-344-77
8 US-10-155-886-49
7 US-10-155-886-10
8 US-10-155-886-11
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (93)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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, OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y Sequence 1340, Application US/09764864

| Patent No. US20020132753A1
| Patent No. US20020132753A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al.
| TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
| TILLE OF INVENTION: NUMBER: US/09/764,864
| CURRENT APPLICATION NUMBER: US/09/764,864
| CURRENT FILING DATE: 2001-01-17
| Prior application data removed - consult PALM or file wrapper
| NUMBER OF SEQ ID NOS: 1792
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 1340
| LENGTH: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 891, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
ITILE OF INTERPRESSOR NICHEL ACIDE, and Antibodies
FILE REPERENCE: PTZ23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 30.1%; Score 56.5; DB 10; Best Local Similarity 39.3%; Pred. No. 7.9; Matches 11; Conservative 5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 188; DB 12;
; Pred. No. 5.5e-16;
0; Mismatches 0;
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       APPLICANT: Xiang, Zhaoying
APPLICANT: Xie, Qing
APPLICANT: Rich, Ging
APPLICANT: Rich, Safia K.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50029
CURRENT PILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: UG/10/312,088
CURRENT FILING DATE: 2000-6-22
PRIOR APPLICATION NUMBER: 60/213,161
PRIOR PILING DATE: 2000-06-22
PRIOR PILING DATE: 2000-06-22
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PSESEG FOR WINDOWS VERSION 4.0
SOFTWARE: PSESEG FOR WINDOWS VERSION 4.0
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Best Local Similarity 100.0%;
Matches 32; Conservative 0;
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ORGANISM: Homo sapiens
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US-09-764-864-891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
## APPLICANT: Deng, Bijia

TITLE OF INVENTION: TYPE 2 CYTOKINE RECEPTOR AND NUCLEIC ACIDS ENCODING

TITLE OF INVENTION: SAME

FILE REPERRACE: 22058-532

CURRENT APPLICATION NUMBER: 00/2-01-14

PRIOR PPLING DATE: 2001-01-12

PRIOR APPLICATION NUMBER: 60/267021

PRIOR PPLING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-13

NUMBER OF SEQ ID NOS: 39

SOPTWARE: PATENTIN VOF: 2.1

SEQ ID NO 4

LENGTH: 263
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100.0%; Pred. No. 5.5e-16;
iive 0; Mismatches 0;
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Cogswell, John P.
Kabnic, Karen S.
Lai, Ying-Ta
Martensen, Shelby A.
Murdock, Paul R.
Smith, Randall F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 32; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 32; Conserv
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APPLICANT: Cogswel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
US-10-312-088-42
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NAME/KEY: SITE
LOCATION: (11)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (19)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SITE
1 LOCATION: (45)
2 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-891-3345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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; Publication No. US20030077808A1
; Publication No. US20030077808A1
; GENERAL INPORMATION:
    APPLICANT: Rosen et al.
; TITLE OF INVENTION: NUMBER: US/09/764,891
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3345
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                                           CREATURE:
CREATURE:
COTHER INFORMATION: MAP TO ACO06249.1
COTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.64
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.68
OTHER INFORMATION: EXPRESSED IN PUNG, SIGNAL = 0.83
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.79
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.79
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.79
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.79
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.79
US-09-864-761-43449
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Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.7%; Score 52; DB 9; Length 20;
52.4%; Pred. No. 6.5;
tive 1; Mismatches 7; Indels
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Publication No. US20030219741A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 HOKPSGCWQHISCNFPGCRTL 30
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APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.7%;
ilarity 42.1%;
Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
US-09-764-891-3345
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US-10-094-749-1942
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APPLICANT: PRAME, DAVIG R.

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Chen, Wencheng

ITILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROREAY CHEN PROBES USEFUL FOR ITILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID FROBES USEFUL FOR ITILE OF INVENTION: GENE EXPERSSION ANALYSIS BY MICROREAY CHEN PROBLEM FILLS OF INVENTION: GENE EXPERSSION ANALYSIS BY MICROREAY CHEN PROBLEM FILLS OF INVENTION: GENE EXPENSE OF SOLI-GS-23 GOOD-GS-26 GOOD-GS-27 GOOD-GS
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CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 891
LENGTH: 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 43449
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30.1%; Score 56.5; I
Best Local Similarity 39.3%; Pred. No. 27;
Matches 11; Conservative 5; Mismatches
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                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-891
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Sequence 33, Application US/10188012
Publication No. US20030124114A1
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CCATION: (1)...(378)
OTHER INFORMATION: TIM-4, allele 1
US-10-188-012-33
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Best Local Similarity 40.0%;
Matches 8; Conservative 5
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FEATURE:
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Best Local Similarity
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                                                                                                                                     APPLICANT: SEEL, MACHIENO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSURA, MOTOVUKI
APPLICANT: OTSURA, MOTOVUKI
APPLICANT: MASUHO, YASUHIKO
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 1942
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Best Local Similarity 43.5%; Pred. No. 35;
Matches 10; Conservative 1; Mismatches
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PRIOR APPLICATION NUMBER: JP 99/377484

PRIOR FILING DATE: 1999-12-16

PRIOR FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: JP 00/159162

PRIOR PLING DATE: 2000-04-07

PRIOR PLING DATE: 2000-08-03

PRIOR PRIOR PLING DATE: 2000-08-03

NUMBER OF FILING DATE: 2000-08-03

SOFTWARE: Patentin ver. 3.0

SQT IN NO 5085
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APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: GEBA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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Publication No. US20020197605A1
GENERAL INFORMATION: APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5085
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                                                                                                            TAMECHIKA, ICHIRO SEKI, NAOHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAYASHI, MIKIRO
OCHIAI, KEIKO
                  HIO, YURI
OTSUKA, KAORU
NAGAI, KEIICHI
                                                                                      RYOTARO
ISONO, YUUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-1942
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APPLICANT: Uneten, Dale T.
APPLICANT: Dekruyff, Rosemarie
APPLICANT: Ruchroo, Vijay
APPLICANT: Freeman, Gordon J.
TITLE OF INVENTION: T Cell Regulatory Genes and Methods of
TITLE OF INVENTION: Use Thereof
FILE REPERENCE: STAN-235
CURRENT APPLICATION NUMBER: US/10/188,012
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/302,344
PRIOR PILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
TYPE: PRI
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Pred. No. 66;
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                                                                                                                                                                                                                                                                                      Sequence 65, Application US/0973907;
Patent No. US20010012889A1;
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TILLE OF INVENTION: 36 Human Secreted Proteins
FILE REFRENCE: P2022P1
CURRENT APPLICATION NUMBER: US/09/739,907.
CURRENT FILING DATE: 1999-07-07;
PRIOR FILING DATE: 1999-07-07;
PRIOR APPLICATION NUMBER: 60/070,567
PRIOR FILING DATE: 1998-01-07;
PRIOR FILING DATE: 1998-01-07;
PRIOR FLILNG DATE: 1998-01-07;
PRIOR FLILNG DATE: 1998-01-07;
PRIOR FLILNG DATE: 1998-01-07;
PRIOR FILING DATE
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33 YAAAWESAHQLKATSQEVFSCEFLGCR 59
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Gaps

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Query Match 27.1%; Score 51; DB 11; Length 379; Best Local Similarity 40.0%; Pred. No. 1.3e+02; Matches 8; Conservative 2; Mismatches 10; Indels
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Pred. No. 3.1e+02;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 48, Application US/09984130
| Sequence 48, Application US/09984130
| Publication No. US20030055231A1
| GENERAL INFORMATION:
| APPLICANT: NI et al. |
| TITLE OF INVENTION: 12 Human Secreted Proteins |
| PRICE REFERENCE: PF489F2 |
| CURRENT FILING DATE: 2001-10-29 |
| PRICE APPLICATION NUMBER: 09/84,130 |
| CURRENT FILING DATE: 2000-10-30 |
| PRICE PREDICATION NUMBER: 60/243,792 |
| PRICE PRILING DATE: 2000-04-18 |
| PRICE APPLICATION NUMBER: 60/18,407 |
| PRICE PRILING DATE: 1999-10-27 |
| PRICE PRILING DATE: 1999-10-27 |
| PRICE PRILING DATE: 1999-10-27 |
| PRICE PRILING DATE: 1999-10-28 |
| NUMBER OF SEQ ID NOS: 149 |
| SEQ ID NO 48 |
| LENTH: 995 |
| LENTH: 995
                                                                                                                                                                        NAME/KEY: SITE
LOCATION: (379)
// OTHER INFORMATION: Xaa equals stop translation
US-09-813-153-139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: December 12, 2003, 12:24:05
Job time : 5.85763 secs
                                                                                                                                                                                                                                                                                                                                                                                                           9 SHOKPSGCWOHISCNFPGCR 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 SHNSNSMCWGKDQCPYSGCK 65
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Best Local Similarity 50.0%;
Matches 9; Conservative
                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NUMBER OF SEC
SOFTWARE: Pat
SEC ID NO 138
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     Gaps
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                                                                                                                                                                                                             Sequence 35, Application US/10188012
| Publication No. US20030124114A1
| GENERAL INPOMATION:
| APPLICANT: Unctsu, Dale T.
| APPLICANT: Unetsu, Dale T.
| APPLICANT: Unetsu, Dale T.
| APPLICANT: Exemen, Gordon J.
| TITLE OF INVENTION: T Cell Regulatory Genes and Methods of TITLE OF INVENTION: Use Thereof
| FILE REPERENCE: STAN-235
| CURRENT APPLICATION WUMBER: US/10/188,012
| FILE REPLICATION UNUBER: 60/302,344
| PRIOR APPLICATION UNUBER: 60/302,344
| NUMBER OF SEQ ID NOS: 36
| SOFFWARE: PSECSE FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.1%; Score 51; DB 15; Length 378; 40.0%; Pred. No. 1.38+02; tive 2; Mismatches 10; Indels
     10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 118, Application US/09813153
Fublication No. US20030045459A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 67 Human secreted proteins
FILE REFERENCE: PZ023
CURRENT FAILIGNION NUMBER: US/09/813,153
CURRENT FILING DATE: 2001-03-21
FRIOR FILING DATE: 1999-07-29
FRIOR FILING DATE: 1999-07-29
FRIOR FILING DATE: 1999-01-30
FRIOR FILING DATE: 1998-01-30
  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1)...(378)
OTHER INFORMATION: TIM-4, allele 2
                                                  9 SHOKPSGCWOHISCNFPGCR 28
                                                                                  46 SHNSNSMCWGKDQCPYSGCK 65
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  8; Conservative
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ORGANISM: H. sapiens
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NAME/KEY: VARIANT
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  Matches
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Gaps

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RESULT 1
AAU09186
                                                                                          December 12, 2003, 12:15:52 ; Search time 8.13559 Seconds (without alignments) 624.325 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
                                                                                                                                                                                                                                                                                                                    1107863
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                              1 MPSCSMKSSHOKPSGCWQHISCNFPGCRTLAK 32
                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                 1107863 segs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                US-10-047-264A-4_COPY_67_98
                                                             - protein search, using sw model
                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
               Copyright
                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                Scoring table:
                                                              OM protein
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                                                                                            Run on:
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ion	RO19598	e recept	ytokine	ytokine	L-TIF/II	ovel sec	ovel pol	ovel sec	נטת ופיזט
Description	Human PRO195	Cytokine	Human C	Human C	Human I	Human novel secret	Human no	Human no	Unman n
UMMARIES	86	66	82	21	24	87	26	38	7.0
υ ₀ Α		ABJ104	AA0173	AAE173	AAU803	AAU16387	ABUS54	AAU159	ABITAGO
DB	22	23	23	23	23	22	24	22	24
* Query Match Length DB I	262	263	263	263	263	103	103	399	399
% Query Match	100.0	100.0	100.0	100.0	81.4	30.1	30.1	30.1	20.5
Score	188	188	188	188	153	56.5	56.5	56.5	7,77
Result No.	-	7	m	4	5	9	7	æ	σ

Human nucleic acid Protein encoded by	Human tumour suppr	Propionibacterium	Human liver peptid	Peptide #5932 enco	Human brain expres	Human bone marrow	Peptide #5902 enco	Human peptide enco	Human reproductive	Propionibacterium	Hepatitis GB virus	Human apolipoprote	Novel human diagno	C glutamicum prote	Human secreted pro	Propionibacterium	Human secreted pro	Human polypeptide	Amino acid sequenc	Amino acid sequenc	Human secreted pro	Mycobacterium spec	Novel human diagno	Mycobacterium spec	P-superfamily cono	P-superfamily cono	P-superfamily cono	Conus sp conotoxin		Novel human diagno	8	Arabidopsis thalia	thali	8	
AAE25288 .		AAU42091	ABG53249	ABB38426	AAM59036	AAM71567	AAM31865	ABG41379	AAM94687	AAU51635	AAR94345	ABB11527	ABG08112	AAG91331	ABB11089	AAU53344	AAY38395	AAM39027	ABP70446	ABP70447	AAY25768	AAY04799	ABG11413	AAY04813	AAU03908	AAU03915	AAU03920	ABG99374	AAU60034	ABG03615	AAG18278	AAG49802	AAG18277	AAG49801	
23	22	22	22	22	22	22	22	23	22	55	16	22	22	22	22	22	20	22	24	24	20	20	22	20	22	22	22	53	55	22	51	7	21	21	
668	761	105	20	20	20	20	20	20	63	308	3164	1008	1013	63	124	144	183	378	378	378	379	148	154	234	27	88	88	83	358	443	190	192	307	309	
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56.5	5 0	53	52	52	52	25	52	52	52	25	52	51.5	51.5	51	51	51	51	51	51	51	51	50.5	50.5	50.5	20	20	20	20	20	20	49.5	œ.	•	•	
01	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	50	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

AAU09186 standard; Protein; 262 AA

AAU09186;

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Human; PRO19598; clone DNA145887; immune-related disorder; inflammatory disorder; infectious disorder; immunodeficiency disorder; autoimmune disorder; renal disease; demyelinating disease; skin disease; neoplasia; transplantation associated disease; immunosuppressive; anti-inflammatory; antiasthmatic; antidiabetic.
                                                                                                                                                                                                                                                 21..262
/label= Mature_PRO19598_polypeptide
                                                                                                                                                                                                                 /note= "N-myristoylation site"
                                                                                                                                                                                                                                        "N-myristoylation site"
                                                                                                                                                                                                                                                                                                  /note= "N-glycosylation site"
170..173
                                                                                                                                                                                                                                                                        55..58
/note= "N-glycosylation site"
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/label= Signal_peptide
                                                                                                                                                                    Location/Qualifiers
                                                       Human PRO19598 polypeptide.
                                 (first entry)
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/note=
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                                                                                                                                                Homo sapiens
                                 16-JAN-2002
                                                                                                                                                                                Peptide
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The invention relates to an isolated type 2 cytokine receptor family (CRF2-12) nucleic acid molecule encoding a polypeptide with amino acids 21-66 of a 231 residue amino acid sequence, given in the specification, or its complement. The compositions and methods of the present invention are useful for diagnosing, screening and treating disorders associated with abnormal CRF2-12 activity such as autoimmune diseases like rheumatoid archritis, multiple sclerosis and inflammation. This sequence represents a cytokine receptor family 2 (CRF2-12) protein relating to the
                                                                                                                                    Immunosuppressive, antirheumatic, antiarthritic, neuroprotective; antiinflammatory, interleukin-antagonist-22, gene therapy, interferon-antagonist-alpha; interferon-antagonist-beta; interferon-antagonist-clammatory, cytokine receptor family 2; CRF2-12; autoimmune disease; rheumatoid arthritis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, cytokine receptor; immune disease; psoriasis; cancer; infection; rheumatoid arthritis; multiple sclerosis; Crohn's disease; ulcerative colitis; transplant rejection; abortion; antipsoriatic; immunosuppressive; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiulcer; cytostatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated CRF2-12 nucleic acid encoding a polypeptide, useful for diagnosing and treating disorders with abnormal CRF2-12 activity such as autoimmune diseases like rheumatoid arthritis, multiple sclerosis
                                                                     Cytokine receptor family 2 (CRF2) related protein SEQ ID No 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 188; DB 23;
; Pred. No. 1.6e-17;
0; Mismatches 0;
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100.0%;
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П
21-NOV-2002 (first entry)
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hes 32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200266647-A2
                                                                                                                                                                                                                                                                                                                    inflammation.
                                                                                                                                                                                                                                                                                                                                                                                       Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to the isolation of 9 novel human PRO polypeptides and the CDNA sequences (AAS15360-AAS15368) encoding them. The provel PRO polypeptides include PRO1356, PRO1368, PRO1368, PRO1364, PRO3444, PRO3151, PRO4322, PRO9964, PRO1006 PRO1359. PRO1569, PRO1364, PRO3151, PRO4322, PRO9964, PRO1006 PRO19598. The CDNA sequences encoding these PRO polypeptides have been designated as clones DNA64886-1601, DNA64903-1553, DNA84318-2520, DNA95997, DNA89273, DNA89273, DNA9223-2567, DNA96903-1553, DNA101921 and DNA145887 respectively.

Compositions (e.g. vaccines) containing PRO polypeptides and methods of using these compositions are useful in the treatment and diagnosis of imflammatory disorders (e.g. otdeoarthritis), infimume-mediated inflammatory disorders (e.g. otabates mellitus), infectious disorders (e.g. diabates mellitus), infectious disorders (e.g. theumatoid arthritis), immune-related renal diseases (e.g. cirrhosis), demyelinating diseases of the peripheral or central nervous system (e.g. diallalan-Barre syndrome), immune-mediated cases contact dermatitis), neoplasias and transplantation associated diseases. The polymuleotide sequences of the invention may be contact the polymuleotide sequences of the invention may be contact the movel human and the contact the novel human and the contact the contact the contact the novel human and the contact the contact
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding PRO polypeptides, useful for detecting and treating immune related diseases and disorders in mammals including autoimmune diseases, inflammatory diseases and asthma -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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100.0%; Pred. No. 1.5e-17;
iive 0; Mismatches 0;
                                                                                                                                                                                                             /note= "N-myristoylation site"
   "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Godowski PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MFSCSMKSSHQKPSGCWQHISCNFPGCRTLAK 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "N-glycosylation
                                                                                                                                    "N-glycosylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; Fig 18; 122pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-191015P
                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001; 2001WO-US06666
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220..225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-625876/72.
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                                 Modified-site
                                                                                                   Modified-site
                                                                                                                                                                     Modified-site
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24-AUG-2000;
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Eaton DL, Tumas D, V

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Gaps

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Sequence

PRO

Query Match

Best Loc Matches

ABJ10499

RESULT 2 ABJ10499

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Length 263; IndelB Martensen SA; Xie Q, Rizni SK;

Weiss B,

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The invention relates to secreted and membrane-associated polypeptides and polymucleotides. The sequences of the invention are useful in diagnostic assays for detecting diseases associated with inappropriate activity or levels of these polymucleotides, and in identifying their activity or levels of these polymucleotides, and in identifying their agonists and antagonists that are potentially useful in therapy. The sequences of the invention are useful as vaccines for inducing timention are useful as vaccines for inducing timention are useful as vaccines, heematopoietic disporders, infections, autoimmune disorders, heematopoietic disporders, nound healing disorders, cholesteryl ester storage disease, infections, altherimer's disease, multiple sclerosis, inflammation, congenital muscular dystrophy, junctional epidermolysis (viral and bacterial infections, Alzheimer's disease, asthma, arthritis, allergies, schizophrania, spg44224PRROa-associated disorders, consistential and bacterial infections, Alzheimer's disease, transplant rejection, congenital infections, Alzheimer's disease, transplant rejection, allergies, schizophrania, spg44224PRROa-associated disorders, conference including parasupranuclear palsy, myotonic dystrophy, depretension, anxiety disorders and aleep disorders are prisorders including parasupranuclear palsy, myotonic dystrophy, disorders including chronic obstructive pulmonary disease including chronic obstructive pulmonary disease including chronic obstructive pulmonary disease including chronic construction and adult respiratory distress syndrome, including and adult respiratory diseases syndrome, including acute and chronic creal failure, glomerulonome, cystinuria, skeletal muscle disorders including parte and chronic creal failure, glomerulonome, cystinuria, skeletal muscle disorders including parte and chronic creal failure, glomerulonome, cystinuria, skeletal muscle disorders including parte and chronic renal failure, glomerulonome, cystinuria, skeletal muscle disorders including parte and c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel secreted and membrane-associated polypeptides and polynucleotides useful for preventing, ameliorating or correcting dysfunction or disease including diabetes, cancer, hypertension and growth
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Pred. No. 1.6e-17;
                                                                                                                                                                                                                                                                                                                                    , Kabnic KS, Lai Y,
Strum JC, Xiang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MFSCSMKSSHQKPSGCWQHISCNFPGCRTLAK 32
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                                                                                                                                                                                                                           (SMIK ) SMITHKLINE BEECHAM CORF
(SMIK ) SMITHKLINE BEECHAM PLC.
(GLAX ) GLAXO GROUP LTD.
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Smith RF, 1
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Best Local Similarity
Matches 32; Conserv
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WO200198342-A1.
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PR,
                                                 27-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides the protein and coding sequences of 3 diagnosis, of a human cytokine receptor. The sequences can be used in the diagnosis, prevention and treatment of immune diseases, including psoriasis, cancer, chronic/life-threatening infections, rheumatoid arthritis, multiple sclerosis, Crohn's disease, ulcerative colitis and transplant rejection and in reproductive medicine, e.g. for diagnosing abnormal immune reactions which cause abortions. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding soluble cytokine receptor, useful for diagnosis and treatment of e.g. immune disease, also related protein
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                                                                                                                                                                                                                                                                                                                                                                                                                      Assadullah K,
  chromosome 6q24:1-25.2; receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 15; 21pp; German.
                                                                                                                                                                                                                                                            25-SEP-2000; 2000DE-1048626.
17-NOV-2000; 2000DE-1058907.
19-DEC-2000; 2000DE-1064906.
                                                                                                                                                                                                           24-AUG-2001; 2001EP-0250307.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            variant 3 of the invention.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     (SCHD ) SCHERING AG
                                                                                                                                                                                                                                                                                                                                                                                                                            Sabat R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 A.A.
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                                                                                                        EP1191035-A2.
                                                      Homo sapiens
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Sequence

Matches

AAE17321;

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Gaps

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AAU80324

Length 263;

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Human novel secreted protein, Seg ID 1340.
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                                                                                                                         Human, soluble protein, interleukin-TIF/IL-22; IL-TIF/IL-22; IL-22BP;
IL-TIF/IL-22 antagonist.
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84.4%; Pred. No. 8.8e-13;
ive 0; Mismatches 5; Indels (
                                                                       Human IL-TIF/IL-22 binding protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 14; Page 41-42; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                             22-SEP-2000; 2000US-234583P.
03-NOV-2000; 2000US-245495P.
31-JUL-2001; 2001US-0919162.
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Best Local Similarity 84.4%;
Best Local 27; Conservative
                      15-JUL-2002 (first entry)
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                                                                                                                                                                                                      Homo sapiens.
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Human, immunosuppressive, antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; noctropic; cerebroprotective; noctropic; untibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebroaccular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
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2000US-0227182.
2000US-0227009.
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                                                                                                Homo sapiens
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2000US-0232397

1 MFSCSMKSSHQKPSGCWQHISCNFPGCRTLAK 32

ઠે 셤 AAU16387 standard; Protein; 103 AA

(first entry)

07-NOV-2001 AAU16387;

AAU16387 ID AAU1 XX AC AAU1 XX DT 07-F

RESULT 6

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2000US-0237039.
2000US-0237040.
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2000US-0249217.
2000US-0249218.
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The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autofimmune diseases e.g. rheumarcid arthritis, hyperproliferative disorders e.g. rheumarcid arthritis, chyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, orberovascular disorders e.g. corneal infection, and many other disorders e.g. corneal infection, and many other disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to and wound healing and epithelial cell proliferation, to prevent skin aging due to sumburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypetides can also case a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present
                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; SEQ ID No 1340; 980pp; English
                                                                                                                                                                                                                                                                                     Ruben SM;
                                                                          2000US-0251868.
2000US-0251869.
2000US-0251989.
2000US-0251990.
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                                       2000US-0251479.
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N-PSDB; AAS26374.
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06-DEC-2000;
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Gaps

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6 DB 22;

30.1%; Score 56.5; D 39.3%; Pred. No. 4.3; :ive 5; Mismatches

11; Conservative

Query Match Best Local Similarity

Best Local

SSHOKPSG---CWQHISCNFPGCRTLAK 32 11 SSHEETPGSHPLYGHGECKWPGCETLCE

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ò 요 ABU55456 standard; Protein; 103 AA

RESULT 7 ABU55456 Human novel polypeptide #543.

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18-MAR-2003 (first entry)

ABU55456;

Length 103; Indels Human; neural disorder; immune system disorder; renal disorder; muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antiinflammatory;

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The invention relates to human novel polypeptides and their associated polymucleotides. The polypeptides and polymucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end eatage renal disease), hypoproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial infarction) and cancerous diseases. Sequences ABUS4914+ABUS5699 and ABUS5748 represent human novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; cerebroprotective; nootropic; ucurogrotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiovascular disorder; cerebral ischaemia; anglogenesis; nervous system disorder; Alzheimer; sidesase; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
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muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or renal disorders -
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                                                    Claim 11; SEQ ID NO 1340; 402pp; English
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 cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic;
haemostatic; antiarteriosclerotic.
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2000US-229287P.
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N-PSDB; ABX73715.
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C
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Š (HUMA-) HUMAN GENOME SCI INC. Rosen CA, Barash SC,

WPI; 2001-488783/53. N-PSDB; AAS25925.

New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -

Claim 11; SEQ ID No 891; 980pp; English.

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked

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immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. neoplasms of the breast or liver, ardiovascular disorders e.g. orthogonesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungicand ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintenian organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as food additive or preservative to increase or decrease storage as a food additive or preservative to increase or decrease storage as food additive on the invitation, capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; phyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antiinflammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic;
                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                          DB 22; Length 399;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU55007 standard; Protein; 399 AA
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                                                                                                                                                                                                                                                                                          30.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human novel polypeptide #94.
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2000US-217487P.
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                                                                                                                                                                                                                                                                                                                           11; Conservative
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Best Local Similarity
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14-AUG-2000;
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28-JUN-2000;
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The invention relates to human novel polypeptides and their associated polymucleotides. The polypeptides and polymucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lugus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. nasal vestibulitis, nasal polype and sinusitis), reproductive disorders (e.g. congenital heart defects, Ebstein's cardiovascular disorders (e.g. congenital heart defects, Ebstein's cardiovascular disorders (e.g. congenital heart syndrome), renal disorders (e.g. kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. esptic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, cherosclerosis and myocardial infarction) and cancerous diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or renal disorders -
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2000US-236802P.
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RUBEN S M.
BARASH S C.
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Best Local Similarity
Matches 11, Conserv
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(RUBE/)
(BARA/)
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Tumour suppressor gene, IB3089A, DBCCR1, 9q32-33, hypermethylation, Deleted in Bladder Cancer Chromosome Region candidate 1; cancer; bladder cancer; extran cancer; squamous carcinoma; renal cell carcinoma; guamous cell oesophageal carcinoma; prenatal testing; heterozygosity loss.

WO9854318-A1

sapiens

Homo

Protein encoded by tumour suppressor gene IB3089A.

(first entry)

09-MAR-1999

AAW70899;

292 SSHEETPGSHPLYGHGECKWPGCETLCE 319

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AAW70899 standard; Protein; 761

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Human, nucleic acid-associated protein, NAAP-7; neurological disorder, arteriosclerosis; cancer; cell proliferative disorder; atherosclerosis; lymphoma; epilepsy; Alzheimer's disease; developmental; anticonvulsant; autoimmune disorder; AlDS; allergy; anemia; stroke; malaria; leishmania; gene therapy; nootropic; neuroprotective; cerebroprotective; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to nucleic acid-associated proteins (NAAP) and nucleic acids. The nucleic acid and amino acid sequences are useful for diagnosing, treating and preventing cell proliferative e.g. arteriosclerosis, atherosclerosis, lymphoma or cancers), neurological (e.g. epileppy, Alzheimer's disease or stroke), developmental, and autoimmune disorders (e.g. AIDS, allergies, or anaemia) or infections (e.g. malaria, or leishmania), as well as in assessing the effects of exogenous compound on the expression of nucleic acid-associated proteins. The invention is useful in gene therapy. The present sequence is human NAAP-7.
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H, Batra S, Ding L, Lal PG;
AR, Griffin JA, Xu Y, Azimzai Y;
BA, Mason PM, Burford N, Hafalia AJA;
A''~~ BM, Marquis JP, Lee SY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid associated proteins and nucleic acids for diagnosing, treating and preventing cell proliferative (e.g. cancers), neurological (e.g. epilepsy or stroke) or autoimmune disorders (e.g. AIDS) -
                                                                                                            Human nucleic acid-associated protein (NAAP-7).
                                                                                                                                                                                                                               immunosuppressive; protozoacide; antimicrobial.
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/note= "Fork head domain"
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                                                                                                                                                                                                                                                                                               Location/Qualifiers
                 AAE25288 standard, Protein; 668 AA
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Walla NK, Tribouley KM, Yue
Borowsky ML, Lu DAM, Gandhi
Gietzen KY, Tang YT, Warren
Lee EA, Yang J, Gorvad AE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JAN-2001; 2001US-260081P.
16-JAN-2001; 2001US-262302P.
23-JAN-2001; 2001US-263823P.
02-FEB-2001; 2001US-266088P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                              19-DEC-2001; 2001WO-US50256
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                                                                           (first entry)
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Swarnakar A,
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                                              AAE25288;
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                                                                                                                                                                                                                                                                                                              Domain
AAE25288
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The present sequence is encoded by tumour suppressor gene IB3089A, also known as DBCCRI (Deleted in Bladder Cancer Chromosome Region candidate 1). The gene is located at 9432-33. Although the gene is cound in several bladder cancer cells. The DBCCRI gene is involved in the development of sporadic cancer, probably by the deletion of one alled of the gene and/or hypermethylation of the remaining allele, leading to reduced expression of the pene amaining allele, leading to reduced expression of the gene maining allele, are used for treatment or prevention of cancer, particularly bladder, ovarian or skin cancer, squamous carcinoma, renal cell carcinoma or squamous cell oesophageal carcinoma. The DBCCRI protein can be used directly in the same way, or used to raise antibodies and to screen for modulators. The products can be used for diagnosis or cancer, or to indicate predisposition to cancer (including prenatal testing), particularly where this is associated with loss of heterozygosity at 9332-33. Antibodies may also be used for affinity purification, therapeutically as modulator and to detect the protein in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human gene, DBCCR1, associated with bladder and other cancers used for diagnosis, treatment and prevention of cancer
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Pred. No. 52;
5; Mismatches 5; Indele
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N-PSDB; AAV83819.
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RESULT 12

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Score 56.5; DB 23; Length 668; Pred. No. 28; 5; Mismatches 9; Indels 3.

7 Match 30.1%; Local Similarity 39.3%; Nes 11; Conservative

Query Match

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Skeiky YAW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed in multiple tissues but is often down-regulated or silenced in bladder cancer cells due to hypermethylation. The DBCCR1 protein has cytostatic activity. The present sequence and the DBCCR1 promoter can be used in the diagnostic, prophylactic and therapeutic treatment of cancer, especially that which is associated with loss of heterozygosity involving 9q32-33. The cancer includes bladder cancer, squamous carcinoma, skin cancer, renal cell carcinoma, oesophageal and ovarian cancers.
                                                                                            Human; tumour suppressor; IB3089A; cytostatic; promoter; Deleted in Bladder Cancer Chromosome Region candidate 1; DBCCR1; diagnostic; prophylactic; threatment cancer; skin; loss of heterozygosity; LOH; bladder; squamous carcinoma; renal cell; oesophageal; ovarian; chromosome 9q32-33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapa
                                                                                                                                                                                                                                                                                                                                                     useful for identifying a predisposition to
                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a tumour suppressor protein 183089A, also referred as DBCR1 for Deleted in Bladder Cancer Chromosome Region candidate 1. The protein is obtained from a CDNA whose major portion is derived from a clone (Texps5097K12270) isolated from a gridded human foetal brain cDNA library. The DBCCR1 gene was found to be localised at 9932-33 chromosomal region between D951848 and AFWA239XA9. It is
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                                                                          Human tumour suppressor protein IB3089A.
                                                                                                                                                                                                                                                                           (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
           AAY44704 standard; Protein; 761 AA
                                                                                                                                                                                                                                                                                                                                                                cancer or the presence of a tumor
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50.0%;
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                                                     (first entry)
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Best Local Similarity 50.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                      promoter sequence,
                                                                                                                                                                                                                                                                                                Knowles M, Habuchi T;
                                                                                                                                                                                                                                                                                                                     WPI; 2000-171014/15.
N-PSDB; AAZ49891.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            761 AA;
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by p. acnes. The disorders include SAPHO syndrome (synovitis, acne, p. acnes; proventions and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bono, joints and the central nervous system, however it is particularly involved in the inflammatory resence or absence of P. acnes in a patient comprises contacting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention of polypeptides may be used as antigens in the production of antibodies and therefore treated by antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes prosence, by enzyme linked immunosorbent assay (ELISS).
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SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
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44.1%; Pred. No. 13;
iive 3; Mismatches 10,
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                                                                                                                  dermatological; osteopathic; neuroprotectant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-APR-2000; 2000US-199047P.
02-UUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                  20-APR-2001, 2001WO-US12865
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e J, Zhang Y,
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N-PSDB; AASS9516
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Query Match
27.7%; Score 52; DB 2
Best Local Similarity 52.4%; Pred. No. 3.4;
Matches 11; Conservative 1; Mismatches
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Job time : 9.13559 secs
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                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which human liver single exon encoded peptides of the invention.

Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
 Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analysing gene expression in human adult liver
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Pred. No. 3.4;
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                                                                                                                                                                                                                                                                                                                                             Claim 27; SEQ ID No 31897; 658pp; English.
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                                                                                                                                                                                                                                                           Chen W,
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52.4%;
                                                                                                                                             26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
                                                                                                                                                                                21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                         30-JAN-2001; 2001WO-US00664
                                                                                                                                  2000US-0180312
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Best Local Similarity 52.44
Matches 11; Conservative
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                                                          WO200157273-A2
                                    Homo sapiens
                                                                                                                                  04-FEB-2000;
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Human; foetal liver; gene expression; single exon nucleic acid probe.

WO200157277-A2

09-AUG-2001

Homo sapiens

Peptide #5932 encoded by human foetal liver single exon probe.

The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -

Rank DR;

Chen W,

Hanzel DK,

Penn SG,

WPI; 2001-483447/52

(MOLE-) MOLECULAR DYNAMICS INC

26-MAY-2000; 2000US-0207456. 30-UIN-2000; 2000US-0608408. 03-AUG-2000; 2000US-0632366. 21-SEP-2000; 2000US-0234687. 27-SEP-2000; 2000US-023559. 04-OCT-2000; 2000GB-0024263.

30-JAN-2001; 2001WO-US00669

2000US-0180312

04-FEB-2000;

Claim 27; SEQ ID NO 31061; 639pp + sequence listing; English.

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Gaps

5,

Length 20 7; Indels

22;

20 AA;

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December 12, 2003, 12:22:23 ; Search time 6.61695 Seconds (without alignments) 1247.959 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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188
1 MFSCSMKSSHQKPSGCWQHISCNFPGCRTLAK 32
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Maximum Match 100%
Listing first 45 summaries
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2: **sp_archea:**
3: **sp_archea:**
4: **sp_human:**
5: **sp_invertebrate:**
6: **sp_mammal:**
7: **sp_mnc:**
9: **sp_phage:**
10: **sp_phage:**
11: **sp_rodent:**
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SUMMARIES		Description	Q969j5 homo gapien	Q8cxs1 leptospira	Q14230 homo sapien	Q8b121 latino viru	Q8b116 latino viru	Q9ck78 pasteurella	Q96ap5 homo gapien	Q8iw55 homo sapien	Q8ivh2 homo sapien	Q8i8v3 giardia lam	Q8wx56 homo sapien	Q8wu22 homo sapien	Q925t8 rattus norv	O60477 homo sapien	Q90xf6 brachydanio	100 and 1000
SUMM	;	9	96915	Q8CXS1	014230	Q8B121	Q8B116	Q9CK78	Q96APS	QBIW55	Q8IVH2	Q818V3	Q8WX56	Q8WU22	Q925T8	060477	Q90XF6	027.700
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ALIGNMENTS

RESULT 0969.TS	LT 1										
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H	01-DEC-2001	(Tre	(TrEMBLrel.	. 19, 0	Created)						
텀	01-DEC-2001	(TrE	MBLrel	. 19, I	19, Last sequence update)	ence	npqa	te)			
텀	01-MAR-2003	(TrE	(TrEMBLrel.	. 23, 1	ast anno	otati	dn uo	date)			
四四	Soluble cytokine class II receptor, long isoform precursor	kine	class	II rec	eptor,]	ong	isofo	rm pre	cursor		
DΕ	(Interleukin 22-binding protein CRF2-10L).	1 22-	bindin	g prote	in CRF2	101)					
Š	CRF2-S1 OR IL22BP.	L22B	٠ <u>.</u>								
SO	Homo sapiens (Human)	H.			٠		•		•		
ဗ	Eukaryota; Metazoa;	letaz		Chordata;	Craniat	۲. ده:	erteb	rata;]	Craniata; Vertebrata; Euteleostomi;	mi;	
s S	Mammalia; Eutheria;	ther		Primates;	Catarrhini; Hominidae; Homo	ini	HOM	nidae;	Homo.		
S	[1]										
R.P.	SECUENCE FROM N.A.	N W	Ā.								
RC	TISSUE=Placenta;	inta;									
X	MEDLINE=21518574; PubMed=11607789;	8574	, PubM	ed=1160	7789;						
æ	Gruenberg B.H., Schoenemeyer A.,	н.	Schoen	emeyer	Schoenemeyer A., Weiss B., Toschi L., Kunz	35 B.	, Tos	chi L.	, Kunz S.,		
RA A	Wolk K., Asa	dull	ah K.,	Sabat	К.;						
RT	"A novel, soluble homologue of the human IL-10 receptor with	lubl	e homo	logue c	f the h	ımanı	11-10	recept	cor with		
RT	preferential expression in placenta.";	exp	ressio	n in pl	acenta.'	<u>.</u> .					
Z.	Genes Immun. 2:329-334(2001).	2:3	29-334	(2001).							
22	[2]										
RP	SEQUENCE FROM N.A.	N W	A.								
ž	MEDLINE=21286453; PubMed=11390454;	6453	, PubM	ed=1139	0454;						
B	Kotenko S.V.	ĮZ,	otova	L.S., R	irochnit	chen	Х О	V., Est	erova E.,		
RA B	Dickensheets H., Donnelly R.P., Pestka S.;	H	Donne	11y R.F	., Pest)	S.		,			
RT	"Identification, cloning, and characterization of a novel	ion,	cloni	ng, and	charact	eriz	ation	of a	novel soluble	ple	
RT	receptor tha	t pi	nde IL	-22 and	neutra	ızes	118	activi			
Z.	J. Immunol.	166:	7096-7	103 (200	1).						
껆	EMBL; AJ3131	. 62;	CAC856	35.1; -							
絽	EMBL; AY040567; AAK85715.1;	. 67;	AAK857	15.1; -							
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Glycoprotein precursor
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01-MAR-2003
                                                                                                                                                                                                      Latino virus
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01-JUN-2001
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                                                         Q8B121
Q8B121;
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O8B116;
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Horwitz M.S., Boyce-Jacino M.T., Faras A.J.;
Horwitz M.S., Boyce-Jacino M.T., Faras A.J.;
"Novel human endogenous sequences related to human immunodeficiency virus type 1.";
J. Virol. 66:2170-2179(1992).
BMBL; M86246; AAAS8451.1;
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                          Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
NCBL_TaxID=173;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                      Length 263;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.6%; Score 59.5; DB 4; Length 54; 52.2%; Pred. No. 0.19; ive 0; Mismatches 8; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=56601./ Serogroup Icterohaemorrhagiae / Serovar lai;
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                                                                                Indels
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB10475; ABN50326.1; -.
Complete proteome.
SEQUENCE 367 AA; 42467 MW; CICIAAS9DDF69785 CRC64;
  C96ECECSD78AC79B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 AA; 6440 MW; AA56AF67667B3214 CRC64;
                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative rhodanese-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                      100.0%; Score 188; DB 4;
llarity 100.0%; Pred. No. 1.4e-19;
Conservative 0; Mismatches 0;
                                                                                                                                          67 MFSCSMKSSHQKPSGCWQHISCNFPGCRTLAK 98
                                                                                                                     1 MFSCSMKSSHQKPSGCWQHISCNFPGCRTLAK 32
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                                                                                                                                                                                                                                                                 PRT;
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263 AA; 30550 MW;
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01-DEC-2001 (TrEMBLrel. 19,
EHS-2 protein (Fragment).
EHS-2.
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Best Local Similarity 52.2°
Matches 12, Conservative
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Best Local Similarity
                                                         Local Similarity
les 32; Conserv
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SEQUENCE
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Q8CXS1;
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AC 08CX
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MEDLINE=22197098; PubMed=12207889;
Charrel R.N. Feldmann H., Fulhorst C.F., Khelifa R., de Chesse R.,
Charrel R.N.;
"Phylogeny of New World arenaviruses based on the complete coding
sequences of the small genomic segment identified an evolutionary
lineage produced by intrassegmental recombination.";
Biochem. Biophys. Res. Commun. 296:1118-1124(2002).
ERMBL, AFS128130; AAN132959.1; -.
SEQUENCE 515 AA; 59222 MW; AA247F14123831B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                             from the
                                                                                                                                                                                                     Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus NCBI_TaxID=45221;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       515;
                                                                                                                                                                                                                                                                                                       STEAIN=Maru 10924;
Archer A.M., Rico-Hesse R.;
"High Genetic Divergence and Recombination in Arenaviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
31.1%; Score 58.5; DB 12; Length
Best Local Similarity 40.0%; Pred. No. 2.4;
Matches 10; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                     Americas.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ database
EMBL; AF485259; AAN09940.1; -
SEQUENCE 515 AA; 59232 MW; 9A247EC412383128 CRC64;
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  515 AA
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(TrEMBLrel. 23, Last ann
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                                              01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
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PRELIMINARY;
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PRELIMINARY;
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TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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Q818V3
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May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

EMBL; AE006212; AAK03839.1;
HSSP; P00195; ICLE.
InterPro; IPR001450; 4Fe4S ferredoxin.
InterPro; IPR001450; AFe4S ferredoxin.
Pfam; PF00037; fe4f; 3.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.6%; Score 57.5; DB 16; Length 206; 42.9%; Pred. No. 1.4;
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R Pfam; PRO0250; Zf-CZHZ; 1.

R PRINTS; PRO0053; Zf-CZHZ; 1.

R PRINTS; PRO00425; TF FORK—Head; 1.

R PRODOM; PRO0339; FH; 1.

R SWART; SM00339; FN; 1.

R PROSITE; PS50039; FORK HEAD 3; 1.

R PROSITE; PS50039; ZINC_FINGER_CZHZ 1; 1.

R PROSITE; PS60028; ZINC_FINGER_CZHZ 1; 1.

R PROSITE; PS60038; ZINC_FINGER_CZHZ 1; 1.

R PROSITE; PS60038; ZINC_FINGER_CZHZ 1; 1.

R PROSITE; PS60038; ZINC_FINGER_CZHZ 1; 1.
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO16674; APH16874.1; -.
InterPro; IPR001766; TF Fork head.
InterPro; IPR007067; Znf C2H2.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DAX-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein (Fragment).
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30.1%; Score 56.5; DB 4;
Best Local Similarity 39.3%; Pred. No. 3.5;
Matches 11; Conservative 5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                383 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE, PS00198, 4FE4S PERREDOXIN, 1.
PROSITE, PS00190, CYTOCHROME_C; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Conservative
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                             Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome SEQUENCE 206 AA
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                                                                                                                           NCBI_TaxID=747;
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GOOS REPRENTED BRITTED BRITTED
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Daigo Y., Takayama I., Fujino M.A.;
"Isolation, mapping, and characterization of a novel human cDNA differentially expressed in the fundus of W/Wv mutant mice."; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO80747; BACS3809.1; -
SEQUENCE 680 AA, 73488 MW; A63826ED85B24752 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 667;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Glardia lamblia (Glardia intestinalis).
Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
NCBI_TAXID=5741;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC040962; AAH40962.1; -
SEQUENCE 667 AA; 72216 MW; 41ED0AP8996FE17F CRC64;
                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to RIKEN CDNA 1200010K03 gene.
Homo sapiens (Human).
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Fork head-related protein like A.
667 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    742 AA
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30.1%; Score 56.5; D
Best Local Similarity 39.3%; Pred. No. 6;
Matches 11; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 SSHEETPGSHPLYGHGECKWPGCETLCE 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 SSHEETPGSHPLYGHGECKWPGCETLCE 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 SSHQKPSG---CWQHISCNFPGCRTLAK 32
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                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                    01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
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SEQUENCE FROM N.A.
STRAIN=WB;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Habuchi T., Luscombe M., Elder P.A., Knowles M.A.;
"Structure and methylation-based silencing of a gene (DBCCR1) within
candidate bladder cancer tumor suppressor region at 9q32-q33.";
Genomics 48:277-288(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Asari M.;
"Identification and characterization of BRINP, a BMP/retinoic acid-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matsuoka I., Nakatani T., Kawano H., Kobayashi M., Abe A., Arai N.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 29.3%; Score 55; DB 11; Length 760; Best Local Similarity 50.0%; Pred. No. 11; Matches 10; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 29.3%; Score 55; DB 4; Length 761; Local Similarity 50.0%; Pred. No. 11; es 10; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inducible neural-specific protein."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AB051356, BAB55642.1; ...
InterPro; IPR001862; MAC_perforin.
SMART; SM00457; MACPP; 1.
SEQUENCE 760 AA; 88654 MW; 22A30B493BC265D3 CRC64;
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InterPro; IPR001862; MAC_perforin.
SMART; SM00457; MACPF; 1.
SEQUENCE 761 AA; 88790 MW; 59E1B2B3231353E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) BMP/retinoic acid-inducible neural-specific protein.
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                 760 AA
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                                                                   24
                                                                                                            5 SMKSSHOKPSGCWOHISCNF 24
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                                                                   SMKSSHQKPSGCWQHISCNF
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                           RESULT 13
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Slavin I., Touz M.C., Lujan H.D.;
"Control of antigenic variation in Giardia lamblia is mediated by antisense RNA-based silencing system.";
Submitted (WG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY142139; AAN52113.1; -.
SEQUENCE 742 AA; 76679 MW; 94F5EA914EEE465D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to deleted in bladder cancer chromosome region candidate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
BA2804.1 (Deleted in bladder cancer chromosome region candidate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 SCSMKSSHOKPSGCWQHIS-----CNFPGCRTLAK 32
                                                                                                                                                                                                                                                                                                                                                                                                     21;
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                                                                                                                                                                                                                                                                                                      Query Match
30.1%; Score 56.5; DB 5; Length 742;
Best Local Similarity 23.5%; Pred. No. 6.6;
Matches 12; Conservative 8; Mismatches 10; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
29.3%; Score 55; DB 4; Length 320;
Best Local Similarity 50.0%; Pred. No. 4.9;
Matches 10; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Length 228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Babbage A.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL138994; CAD13302.1; -.
NON TER 228 2288 2288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC021560; AM+21560.1; -.
Interpro; IRRO1862; MAC_perforin.
SMART; SM00457; MACPF; 1.
SEQUENCE 320 AA; 37168 MW; 216A4CB3D764C5C3 CRC64;
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Pred. No. 3.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel, 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Gaps

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Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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Development 128:4021-4034(2001).

BEMBL, ARX833531.;

InterPro; IPR007087; Znf C2H2.

Promo: PD000005, zf C2H2; J.

SNART; SM00355, znr C2H2; J.

PROSITE; PS00028; ZINC FINGER C2H2 1; 3.

PROSITE; PS00028; ZINC FINGER C2H2 2; 3.

RHOSITE; PS01057; ZINC FINGER C2H2 2; 3.

RHOSITE; PS01057; ZINC FINGER C2H2 2; 3.

RHOSITE; PS01057; ANG FINGER C2H2 2; 3.

RHOSITE; PS01057; ZINC FINGER C2H2 2; 3.
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29.0%; Score 54.5; DB 13; Length 367;
Best Local Similarity 44.0%; Pred. No. 6.6;
Matches 11; Conservative 3; Mismatches 10; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=21521131; PubMed=11641225;
Tallafuss A., Wilm T.P., Crozatier M., Pfeffer P., Wassef M.,
Bally-Cuif L.;
                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 2), Last annotation update)
Zinc finger buttonhead-related transcription factor 1.
                                                                                                   367 AA.
                                                                                              PRT;
                                                                                              PRELIMINARY;
                                                                                              Q90XF6
Q90XF6;
RESULT 15
790XF
AC 090XF
AC 090XF
DT 01-DE
DT 01
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Search completed: December 12, 2003, 12:27:22 Job time : 8.61695 secs

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December 12, 2003, 12:16:38; Search time 2.06102 Seconds (without alignments) 730.151 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                           OM protein - protein search, using sw model
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US-10-047-264A-4_COPY_67_98 188 1 MFSCSMKSSHQKPSGCWQHISCNFPGCRTLAK 32 Title: Perfect score: Sequence:

127863 segs, 47026705 residues Searched:

BLOSUM62 Gapop 10.0°, Gapext 0.5

Scoring table:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	O8cxsl leptospira	_		7 ratt	_	P02528 rattus norv		conus g												zea	zea			P38605 arabidopsis		_	_	Q98938 gallus gall	~	3 gallūs (_	O54701 rattus norv	6.
SUMMARIES		OI	YV28 LEPIN	CRGF MOUSE	CRGD MOUSE	CRGD RAT	CRGE_MOUSE	CRGE_RAT	CRGF_RAT		YKKA_CAEEL	CD59_PAPSP	CD59_CERAE	NCL1_CAEEL	CX9A_CONTE	P43_XENLA	GRN_HUMAN	ZF37_HUMAN	ACES_ELEEL	BDNF_CHICK	YU20_MOUSE	TRA1 MAIZE	TRA9 MAIZE	RT25_DROME	YMP4_YEAST	CAS1_ARATH	POLS_ONNVG	FSH_DROME	YHE2_YEAST		AF2A SINAL	CATB_CHICK	AFAM MOUSE	NKX2 RAT	YU20_HUMAN
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		Match Length	36	IJ	173	~	~	7	173	88	266	126	128	851	88	365	593	597	633	246	747	806	839	167	519	759	1247	2038	150	408	51	340	611	670	749
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RESULT 2

24.5 956 1 TSP3 MOUSE Q05895 mus musculu 24.5 1253 1 POLS SFV P03315 semliki for 24.5 1254 1 POLS RRVT P08491 rose river 24.5 2148 1 VITI_REDAB Q05503 rose aegyp 24.2 358 1 C4BP_RAT Q05314 rattus norv 23.9 172 1 TASM POVJC Q07394 rhodobacter 23.9 187 1 RXA9_FUGRU Q04250 fugu rubrit 23.9 1 ICEI_SPOFR Q09150 schizcosacch 23.9 302 1 RE14_SCHPO Q09150 schizcosacch 23.9 350 1 YCEA_SALTY Q8zq23 salmonella	Alignments	ST (Rel. (Rel.	. protein imail8. .nterrogans. birochaetes; Spirochaetales; Leptospiraceae; Leptospira. 73;	M N.A. ./ Serogroup Icterohaemorrhagiae / Serovar lai; 8143; PubMed=12712204;	Miao YG., Xu H., Jiang HQ., Jia J., Z., Sheng HH., Yin, Oian Z., Wang SY.	A VA JG., Zhao GP.; Chen Z., A VA JG., Zhao GP.; Zhao GP.; Chen Z., "Unique physiological and pathogenic features of Leptospira II interrogans revealed by whole-genome sequencing."; In Nature 422:888-893 (2003). CI- SIMILARITY: BELONGS TO THE UPP0176 FAMILY. -I- SIMILARITY: Contains 1 rhodanese domain.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)	AE011475; AAN50326.1; MF.00469; -; 1. PR00581; Rhodanese; 1. SM00450; RHODANESE 3; 1. E; PS50206; RHODANESE 3; 1. letical protein; Complete proteome. 159 253 RHODANESE. 1CB 367 AA; 42467 MW; C1ClAAS9DDF69785 CRC64;	32.4%; Score 61; DB 1; Length 367; larity 40.0%; Pred. No. 0.69; Conservative 5; Mismatches 10; Indels 0; Gaps 0;	MKSSHQKPSGCWQHISCNFPGCRTL 30 : : : : ISSCHQCGAKCDRHVNCENPGCHVL 301
44400 20 20 20 20 20 20 20 20 20 20 20 20 2		EPIN BEPIN 9CXSI	hypotnetical protein LA LA3128. Leptospira interrogans. Bacteria; Spirochaetes; NCBI TaxID=173;	[1] SEQUENCE FROM STRAIN=56601 / MEDLINE=225981	Ken SX., Fu Zhang YX., Y Jiang JX., C Zhang Y., Zhu Yao ZJ., She	Xu JG., Zhac "Unique physic interrogans re Nature 422:886 -!- SIMILARITY	This SWISS-PRC between the S the Buropean to see by non-r modified and t entities requi	EMBL, AE011475; AAN50326. HAMAP, MF 00469; -; 1. Pfam; PF0581; Rhodanese; SMOATC; RHOD; 1. PROSITE; PS50206; RHODANE; Hypothetical protein; Component	Query Match Best Local Simila Matches 10; Co	6 MKSSH : 277 ISSCH
		RESULT YV28 L ID X AC Q DT 1		R R R X	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	84	3888888888		Oue Bes Mat	දු පු

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                     Klopp N., Favor J., Loseter J., Lutz R.B., Neuhaeuser-Klaus A., Presect A., Pretsch W., Quinlan R.A., Sandilands A., Presect G.F.J.M., Graw J.;

"Therse murine cataract mutants (Cat2) are defective in different gamma-crystallin genes.";

Genomics 52:152-158(1998)

-!- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS OF THE VERTEBRATE EXE LENS.

-!- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR VERY SIMILAR GREEK KEY MOTIFS.

-!- HISCELLANBOUS: THERE ARE SIX DIFFERENT GAMMA CRYSTALLINS IDENTIFIED IN MOUSE LENS.
                                                                                                                                                                                         MEDLINE-85088487; PubMed-6096855; Breitman M.L., Lok S., Wistow G., Piatigorsky J., Treton J.A., Gold R.J.M., Tsui L.-C.; Westow G., Respectable family of the mouse lens: structural and "Gamma-crystallin family of the mouse lens: structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
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E33755FBE9636969 CRC64;
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MOTIF 2.
CONNECTING PEPTIDE.
MOTIF 3.
                                                                                                                                                                                                                                                                                 evolutionary relationships.";
Proc. Natl. Acad. Sci. U.S.A. 81:7762-7766(1984)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00247; XTALbg; 2.
PROSITE; PS00225; CRYSTALLIN BETAGANMA; 4.
Eye lens protein; Multigene Family; Repeat.
1INIT_MET
                    Gamma crystallin D (Gamma crystallin 1)
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99000834; PubMed=9782080;
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MGD; MG188524, Crygd.
InterPro; IPR001064; Crystallin.
Pfam, PP00030; crystall; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; K02583; AAA37475.1; -.
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                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 3-104 FROM N.A.
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83
86
127
173
                                                            Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR, A02932; CYMSG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 AA;
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                      STRAIN=102 X C3H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=CD-1; TISSUB-Eye;
MEDLINE=92124352; PubMed=1623964;
Goring D.R., Breitman M.L., Tsui L.-C.;
"Temporal regulation of six crystallin transcripts during mouse lens development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                        EYE RES. 54:785-795 (1992).
FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS OF THE VERTEBRATE EYE LENS.
DEVELOPMENTAL STAGE: IN THE EMBRYO, EXPRESSED BY DAY 12 OF GESTATION. MAXIMUM LEVELS ARE FOUND AT DAY 30-40 FOLLOWED BY A RAPID DECLINE.
                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: HAS, A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERY SIMILAR GREEK KEY MOTIFS.
MISCELLANEOUS: THERE ARE SIX DIFFERENT GAMMA CRYSTALLINS
IDENTIFIED IN MOUSE LENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 27.1%; Score 51; DB 1; Length 158; Best Local Similarity 30.8%; Pred. No. 6.2; Matches 12; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158
19339 MW; DD2DB2807404410A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 FSCSMKSSHQKP-----SGCWQ-HISCNFPGCR 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 YECSTDHSNLOPYFSRCNSVRVDSGCWMLYEQPNPAGCQ 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P02528; LCC.
MGD; MGI: 18826; Crygf.
Interpro; IPR001064; Crygf.
Interpro; PR00030; crystall; 2.
PRINTS; PR01367; BGCNSTALLIN.
SMART; SM0247; XTALbg; 2.
PR031TB; P80225; CRYSTALLIN BETACAMMA; 3.
PR031TB; P80215; CRYSTALLIN BETACAMMA; 3.
FEYE lens protein; Multigene Family; Repeat.
                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Gamma crystallin F (Fragment).
                      158 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P04342; 089027;
20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
                    PRT;
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                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                        Mus musculus (Mouse)
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                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                      CRGF MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRGD MOUSE
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SEQUENCE
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CRGD MOUSE
ID CRGD MC
AC P04342;
DT 20-MAR-
DT 20-MAR-
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7
                      Gaps
                      12;
 Score 51; DB 1; Length 173;
Pred. No. 6.8;
27.1%; Score or, 30.8%; Pred. No. 6.8; orive 5; Mismatches 10; Indels
                                                      2 FSCSMKSSHQKP-----SGCWQ-HISCNFPGCR 28
                                                                                                               173 AA
                                                                                                                PRT;
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                                                        Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=87060933; PubMed=3783678; MEDLINE=87060933; PubMed=3783678; den Dunnen J.T., Moormann R.J.M., Lubsen N.H., Schoenmakers J.G.G.; "Concerted and divergent evolution within the rat gamma-crystallin
                                                                                                                                                                                                                                                                                                                                                                         Biochimie 76:398-403(1994).
-!- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS OF THE VERTEBRATE EYE LENS.
-!- DOWAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR VERY SIMILAR GREEK KEY MOTIFS.
-!- MISCELLANEOUS: THERE ARE SIX DIFFERENT GAMMA CRYSTALLINS IDENTIFIED IN RAT LENS.
-!- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
                                                                                                                                                                                                                                                                                                                STRAIN=Sprague-Dawley, TISSUE=Lens,
MEDLINE=95151850, PubMed=7849105,
Ooki K., Amuro N., Shimizu Y., Okazaki T.;
"High level expression of rat gamma-D-crystallin in Escherichia
                                                                                                                             MEDLINE=90236114; PubMed=1970548;
den Dunnen J.T., van Neck J.W., Cremers F.P.M., Lubsen N.H.
Schoenmakers J.G.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.1%; Score 51; DB 1; Length 173; 30.8%; Pred. No. 6.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      930B2D42D80F4117 CRC64;
                                                                                                                                                                   "Isolation and characterization of the rat glutamine synthetase-encoding gene."; Gene 87:225-232(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOTIF 1.
MOTIF 2.
CONNECTING PEPTIDE.
          01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
10-SBP-2003 (Rel. 42, Last annotation update)
Gamma crystallin D (Gamma crystallin 2-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPRO01064; Crystallin.
Pfam; PR00030; crystall; 2.
PRINTS; PR01367; BGCRYSTALLIN.
SMART; SM00247; XTALBG; 2.
PROSITE; PS00225; CRYSTALLIN BETAGAMA; 4.
Eye lens protein; Multigene Family; Repeat.
INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOTIF 3.
MOTIF 4.
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                                                                                                                                                                                                                                                                              Mol. Biol. 189:37-46(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M19359; AAA40984.1; -. EMBL; X57169; CAA40458.1; -.
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83
86
127
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HSSP; P02528; 1A5D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
87
128
173 AA;
                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                    family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 104:265-270(1991).
-!- FUNCTION: CYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS
-- FUNCTION: CYSTRALLINS EXE LENS.
-!- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERY SIMILAR GREEK KEY MOTIFS.
--- NEXCELLANEOUS: THERE ARE SIX DIFFERENT GAMMA CRYSTALLINS IDENTIFIED IN MOUSE LENS.
--- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 51, DB 1, Length 173;
Pred. No. 6.8;
5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=(101/E1XC3H/E1)F1; TISSUE=Liver;
MEDLINE=92009223; PubMed=1916296;
Graw J., Coban L., Liebstein A., Werner T.;
"Murine gamma B-crystallin is distinct from murine gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E17410F82B3C39AE CRC64;
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MOTIF 2.
CONNECTING PEPTIDE.
MOTIF 3.
                                         01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 42, Last annotation update)
  173 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S26811; S26811.
HSSP; P02528; 1A5D.
MGD; MGI: 88225; Cryge.
InterPro; IPR001064; Crystallin.
Pfam; PP00030; crystall; 2.
PRINTS; PR01367; BGCRYSTALLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21093 MW;
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  STANDARD;
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Matches 12, Conservative
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                                                                                                                                                           Mus musculus (Mouse)
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173 AA;
                                                                                                               Gamma crystallin E.
                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                              2-crystallin.";
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CRGE MOUSE
P2699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRGE RAT
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84556
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Gaps

12;

10; Indels

5; Mismatches

12; Conservative

Local Similarity

Best Loca Matches

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Pred. No.

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01-MAR-1989 (
01-MAR-1989 (
15-SEP-2003 (
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ID CRGF_RAT
AC P10068;
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MEDLINE=98035705; PubMed=9367641;
Norledge B.W., Hay R.E., Bateman O.A., Slingsby C., Driessen H.P.C.;
"Towards a molecular understanding of phase separation in the lens: a comparison of the X-ray structures of two high Tc gamma-crystallins, gammaE and gammaE, with two low Tc gamma-crystallins, gammaB and
                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116, 10090;
                                                                                                                                                                                                            SPECIES=Rat;
MEDLINE=81091061; PubMed=6294661;
MOOTMABIN R.J.M., den Dunnen J.T., Bloemendal H.,
Schoenmakers J.G.G.;
"Extensive intragenic sequence homology in two distinct rat lens
gamma-crystallin cDNAs suggests duplications of a primordial gene.";
Proc. Natl. Acad. Sci. U.S.A. 79:6876-6880(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-68 FROM N.A.
SPECIES=Mouse; TISSUE=Lens;
MEDLINE=86284665; PubMed=3837188;
Lok S., Breziman M.L., Chepelinsky A.B., Piatigorsky J.,
Gold R.J.M., Tsui, L.C.;
"Lens-specific promoter activity of a mouse gamma-crystallin gene.";
Mol. Cell. Biol. 5:2221-2230(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISCELLANEOUS: THE TWO SEQUENCES SEEM IDENTICAL. WHAT IS KNOWN GAMMA-E IN RAT IS CALLED GAMMA-2 IN MOUSE. THERE IS ANOTHER GAMMA-E SEQUENCE IN MOUSE. SEQUENCE IN MOUSE. SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                      MEDLINE-84114867; PubMed-6319707; Mulleners L., Andreoli P., Moormann R.J.M., den Dunnen J.T., Mulleners L., Andreoli P., Bloemendal H., Schoenmakers J.G.G.; "Strict co-linearity of genetic and protein folding domains in an intragenically duplicated rat lens gamma-crystallin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXP. E9 Reg. 65:609-610(1997).

-!- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS
OF THE VERTEBRATE EYE LENS.
-!- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR VERY SIMILAR GREEK KEY MOTIFS.
-!- MISCELLANBOUS: THERE ARE AT LEAST SEVEN DIFFERENT GAMMA CRYSTALLINS IDENTIFIED IN MOUSE LENS.
-!- MISCELLANBOUS: THERE ARE SIX DIFFERENT GAMMA CRYSTALLINS IDENTIFIED IN RAT LENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=Mouse;
MEDLINES=8508947; PubMed=6096855;
Breitman M.L. Lok S., Wistow G., Piatigorsky J., Treton J.A.,
Gold R.J.M., Tsui L.-C.;
Gold R.J.M., Tsui L.-C.;
Gould R.J.M., Tsui L.-C.;
Family of the mouse lens: structural and
evolutionary relationships.";
Proc. Natl. Acad. Sci. U.S.A. 81:7762-7766(1984).
                                                                                                                       den Dunnen J.T., van Neck J.W., Cremers F.P.M., Lubsen N.H., Schoenmakers J.G.G.; "Isolation and characterization of the rat glutamine
crystallin E (Gamma crystallin 3-1) (Gamma-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS)
                                                                                                            MEDLINE=90236314; PubMed=1970548;
                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Biol. 171:353-368(1983)
           Rattus norvegicus (Rat), and Mus musculus (Mouse).
                                                                                                                                                             synthetase-encoding gene.";
Gene 87:225-232(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                SPECIES=Rat
                                                                                                                                                                                                                                                                                                                            SPECIES=Rat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gammaD.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                     PIR; A02930; CYRTG1.
PIR; A02931; CYMSG2.
PIR; 156381; 155381.
PDB; 1A5D; 27-MX-98.
InterPro; IPR01064; Crystallin.
PRIM: PR01030; crystall; 2.
PRIMTS; PR01367; BGCRYSTALLIN.
SWART; SM00247; XTALBG; 2.
PROSITE; PS00225; CRYSTALLIN BETAGAWMA; 4.
Bye lens protein; Multigene Family; Repeat; 3D-structure.
INIT MET 0 0 0 00MAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21132 MW; 3F3200E85CB61B02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 YECSTDHSNLQPYFSRCNSVRVDSGCWMLYEQPNFTGCQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                      MOTIF 1.
MOTIF 2.
CONNECTING PEPTIDE.
MOTIF 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 PSCSMKSSHQKP-----SGCWQ-HISCNFPGCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.1%; Score 51; DB 1; illarity 30.8%; Pred. No. 6.8; Conservative 5; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 10, Created)
(Rel. 10, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 AA
                                                                                                                                              EMBL, M19359, AAA40985.1; -. EMBL, J00716; AAA40987.1; -. EMBL, X00271; CAA23073.1; -. EMBL; K02584; AAA03228.1; -. EMBL; M11039; AAA03227.1; -.
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83
· 86
127
173
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1124
1135
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173 AA;
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Best Local Similarity
Matches 12, Conserv
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Conoidea; Conidae; Conus.
                                                                   SEQUENCE FROM N.A.
MEDLINE=20143473; PubMed=10677206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                           ACBI_TaxID=37336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEPTIDE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
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YKKA CAEEL
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          POT SERVICE SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
;
                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                     MEDLINE-87060933; PubMed=3783678; den Dunnen J.T., Moormann R.J.M., Lubsen N.H., Schoenmakers J.G.G.; "Concerted and divergent evolution within the rat gamma-crystallin
                                                                                                                                                                                                                                                                                                                                                                BYNTCHETABE-encoding gene.";
Gene 87:225-232(1990).
-!- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS
OF THE VERTEBRATE EYE LENS.
-!- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR VERY SIMILAR GREEK KEY MOTIFS.
-!- MISCELLANBOUS: THERE ARE SIX DIFFERENT GAMMA CRYSTALLINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spasmodic protein txsa-like protein precursor (Conotoxin Gm9.1). Conus gloriamaris (Glory of the sea).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda; Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                               MEDLINE=90236314; PubMed=1970548;
den Dunnen J.T., van Neck J.W., Cremers F.P.M., Lubsen N.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTIFIED IN RAT LENS.
-!- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 51; DB 1; Length 173; Pred. No. 6.8; 5; Mismatches 10; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40E63B99F75600BD CRC64;
                                                                                                                                                                                                                                                                                                                                               "Isolation and characterization of the rat glutamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 FSCSMKSSHQKP-----SGCWQ-HISCNFPGCR 28
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MOTIF 2.
CONNECTING PEPTIDE.
MOTIF 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001064; Crystallin.
Pfam; PF00030; crystall; 2.
PRINTS: PR01367; BGCRYSTALLIN.
SMART; SM00247; XTALbg; 2.
PR0SITE; PS00225; CRYSTALLIN BETAGAMWA; 4.
Eye lens protein; Multigene Family; Repeat.
INIT_MET
  crystallin F (Gamma crystallin 4-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 MO
83 MO
86 CC
127 MO
173 MO
21210 MW;
                                                                                                                                                                                                   gene family.";
J. Mol. Biol. 189:37-46(1986)
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Q9GU57;
28-PRB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M19357; AAA40988.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.18;
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Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                              Schoenmakers J.G.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E24060; E24060.
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84
87
128
173 AA;
                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                     Rattus norvegicus
                                                                              NCBI_TaxID=10116;
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ID CX9A_CC

AC Q9GU57;

28-FEB-

DT 28-FEB-

DT 15-SFP-

DE Spasmod

OC EUKATY

OC Apogast
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STATIS—Enterol N.Z.

STATIS—Enterol N.Z.

MEDLINE—94150718; PubMed=7906398;

Milson R., Ainscough R., Anderson K., Baynes C., Berks M.,

Milson R., Ainscough R., Anderson K., Frasten J., Cooper J., Coulson A.,

Craxton M., Dear S., Du Z., Durbin R., Favello A., Frasten A.,

M. Huton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,

Latreille P., Lightning J., Lloyd C., Mortinore B., O'callaghan M.,

Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,

Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,

Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,

Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Lirazan M.B., Hooper D., Corpuz G.P., Ramilo C.A., Bandyopadhyay P., Cruz L.J., Olivera B.M.; "The spaemodic peptide defines a new conotoxin superfamily."; Biochemistry 39:1583-1588(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                           Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROBABLE.
AMIDATION (G-88 PROVIDE AMIDE GROUP)
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SPASMODIC PROTEIN TX9A-LIKE PROTEIN.
PROBABLE.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDB; 1IXT; 28-JAN-03.
Toxin; Signal; Amidation; Cleavage on pair of basic residues;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical zinc finger protein CO2F5.12 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 50; DB 1; Length 88; Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C82818A55CBC44E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PROBABLE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SCNNSCÓSHSDCASHCICTFRGC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF193511; AAG28407.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.5%;
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Q95QY7;
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60
87
78
83
83
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HSSP; P13987; 1CDS.
HSSP; P13987; 1CDS.
InterPro; IPR003532; Ly-6 CD59.
InterPro; IPR001254; Ly-6 CD59.
InterPro; IPR001254; Ly-6 CD59.
ProDom; PD003128; Ly-6 CD59; 1.
ProDom; P0003128; Ly-6 CD59; 1.
SWART; SW00134; Ly-1.
PROSITE; PS00983; LX6 UPAR; 1.
PROSITE; PS00983; LX6 UPAR; 1.
Antigen; Glycoprotein; GPI-anchor; Signal.
     send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 CWQHISCNFPGCRTLAK 32
                                                 EMBL; 122862; AAA74127.1; -. PIR; 136914; 136914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 CWKFANCNFNDISTLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 47.1 tes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                            CHAIN
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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CD59_CERAE
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       8
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                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L14745; AAK71355.1; -.
Wormbep; C02F5.12; CE26744.
InterPro; IPR007087; Znf C2H2.
SWART; SM00355; ZnF C2H2; Z.
PROSITE; PS00028; ZINC FINGER C2H2 1; 1.
PROSITE; PS50157; ZINC FINGER C2H2 2; FALSE NEG.
Hypothetical protein; Zinc; Metal-binding; Zinc-finger; DNA-binding;
.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CDS9 glycoprotein precursor (Membrane attack complex inhibition factor) (MACIF) (MAC-inhibitory protein) (MAC-IP) (Protectin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                  the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 180 C2H2-TYPE.
266 AA; 29989 MW; 8293081EDDD0D00D8 CRC64;
                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: Contains 1 C2H2-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.3%; Score 49.5; I
45.5%; Pred. No. 16;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LESSHAN----YVITCNFPGC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 MKSSHQKPSGCWQHISCNFPGC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 45.5
tes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                     Waterston R.; Submitted (OCT-2001) to
                                               Nature 368:32-38(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclear protein.
ZN FING 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD59_PAPSP
                                                                                                   REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
CD59_PAPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPRESENTATION OF THE PRICE OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ठ
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ö

Score 49; DB 1; Length 126; 7900FF937871EBDC CRC64;

13716 MW;

26.1%;

Pred. No. 9.2;

80

CD59 GIYCOPROTEIN.
REMOVED IN MATURE FORM (BY SIMILARITY).
UPAR/ILV6.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
GPI-ANCHOR (BY SIMILARITY).

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    -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By

                                                                                                                                                                                                                                                                                                                 MEDLINE-95104908; PubMed=7528724; Padotw W.V., Rodor W.L., Rollins S.A., Blanco-Caron S., Burton W.V., Guilmette E.R., Rocher R.P., Zavoico G.B., Squinto S.P.; Primate terminal complement inhibitor homologues of human CD59."; Immunogeneetics 41.51.51(1995).
-i- PUNCTION: POTENT INHIBITOR OF THE COMPLEMENT MEMBRANE ATTACK COMPLEX (MAC) ACTION. ACTS AT OR AFTER THE C58-8 STAGE OF MAC
                                                                                                                                                               Cercopithecus aethiops (Green monkey) (Grivet).

Eukaryota, Metazoa, Chordata, Graniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CDS 91ycoprotein precureor (Nembrane attack complex inhibition factor) (MACIF) (MAC-inhibitory protein) (MAC-IP) (Protectin).
128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
-!- SIMILARITY: Contains 1 UPAR/Ly6 domain.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L22863; AAA74126.1; -.
PIR; I36894; I36894.
STANDARD;
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          NCBI_TaxID=9534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASSEMBLY.
CERAE
CD59 CE
Q28216;
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SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By

similarity).
-!- SIMILARITY: Contains 1 UPAR/Ly6 domain.

MEDLINE=95104908; PubMed=7528724; Padot W.L., Rollins S.A., Bianco-Caron S., Burton W.V., Guilmette B.R., Rother R.P., Zavoico G.B., Squinto S.P.; Primate terminal complement inhibitor homologues of human CD59."; Immunogenetics 41:51-51(1995).
-1- FUNCTION: POTENT INHIBITOR OF THE COMPLEMENT MEMBRANE ATTACK COMPLEX (MAC) ACTION. ACTS AT OR AFTER THE C5B-8 STAGE OF MAC

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae, Cercopithecinae, Papio.

Papio sp. (Baboon).

SEQUENCE FROM N.A. NCBI_TaxID=61183;

PROPEP LIPID DOMAIN

CHAIN

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                          (5S RNA) TRANSCRIPTION.
SUBCELLULAR LOCATION: Cytoplasmic.
TISSUB SPECIFICITY: PRESENT IN CELLS IN WHICH NUCLEOLI ARE ABSENT,
AND ABSENT FROM LARGE CELLS IN WHICH NUCLEOLI ARE PROMINENT.
DEVELOPMENTAL STAGE: ABUNDANT IN EARLY EMBRYOS CELLS AND THEN
RAPIDLY DIMINISHES DURING DEVELOPMENT.
        TRANSCRIPTION FACTOR TO INHIBIT RNA POLYMERASE I (RRNA) AND III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The spasmodic poptide defines a new conotoxin superfamily.";
Biochemistry 39:1583-1588 (2000).
--- FUNCTION: Intracranial injection into mice of 10 pmol/g of the peptide induces running in circles and hyperactivity. At higher doses (50 pmol/g), the mice exhibit running and climbing symptoms for close to one hour. Between 130 and 150 pmol/g, characteristic "spasmodic" symptomatology is elicited. A hand clap would make mice jump high and start running rapidly. When exposed to a loud hand clap, or if the cage cover were dropped, the mice lose motor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20143473; PubMed-10677206;
Lirazan M.B., Hooper D., Corpuz G.P., Ramilo C.A., Bandyopadhyay P.,
Cruz L.J., Olivera B.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 SASSTSSHÖVPSLGGKQSPDSMMLGSGKRSVLCLQHRASELVFFCVSCNLAICR 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 SCSMKSSHQKPS-----ISCNFPGCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Mollusca; Gaetropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., SEQUENCE OF 61-87, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 49; DB 1; Length 851;
Pred. No. 53;
1; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
59-FEB-2003 (Rel. 44) Last annotation update)
Conus textile (Cloth-of-gold cone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166FDC4623AE494C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COILED COIL (POTENTIAL).
POLY-SER.
                                                                                                                                                      -1- SIMILARITY: Contains 2 B box-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00355; ELC..., PROSITE; PS50119; ZF_BBOX; 2.
Zinc-finger; Repeat; Metal-binding; Coiled coil.
ZN FING 127 174 B BOX-TYPE 1.
361 B BOX-TYPE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; 844890; 844890.

WormPep; ZK112.2; CE00373.

InterPro; IPR003649; Bbox.C.

InterPro; IPR001258; NHL.

InterPro; IPR000315; Znf_Bbox.

Pfam; PF01436; NHL; S.f.

Fam; PF00643; zf_Bbox; 2.

SMART; SM00336; BBOX; 2.
                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF047027; AAC14263.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91954 MW;
                                                                                                                                                                                                                                                                                                                                                                                                   L14324; AAA28185.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 26.1
Best Local Similarity 29.6
Matches 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261
336
194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    851 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rissum=Venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CX9A CONTE
Q9GU58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
CX9A_CONTE
           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
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-1- FUNCTION: INVOLVED IN THE REGULATION OF RIBOSOMAL RNA SYNTHESIS

AND CELL GROWTH. MAY BE AN INHIBITOR OF THE LEVEL OF BIOSYNTHETIC

AND THUS WITHIN A CELL BY REPRESSING THE PRODUCTION OF RIBOSOMES,

AND THUS THE CAPACITY FOR PROTEIN SYNTHESIS. MIGHT ACT DIRECTLY AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Ncl-1 is required for the regulation of cell size and ribosomal RNA synthesis in caenorhabditis elegans."; J. Cell Biol. 140:1321-1329(1998).
                                                                                                                                                                                                                  REMOVED IN MATURE FORM (BY SIMILARITY).
GPI-ANCHOR (BY SIMILARITY).
UPAR/LY6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NGBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                               . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., POSSIBLE FUNCTION, AND SUBCELLULAR LOCATION STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 49; DB 1; Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   9778DEF7F7F05152 CRC64;
                                                                                                                                                                                            CD59 GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
HSSP, P13987, 1CDS.
InterPro; IPR003632; Ly-6 CD59.
InterPro; IPR001526; LY6 UPAR.
FERM; PP00021; UPAR LY6; 1.
ProDom; PD003128; Ly-6 CD59; 1.
SWART; SM00134; LU; 1.
PR0SITE; PS00983; LV5 UPAR; 1.
ARLigen; Glycoprotein; GPI-anchor; Signal.
SIGNAL.
                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       851 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                          BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B-box type zinc-finger protein ncl-1.
NCL-1 OR ZK112.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98177161; PubMed=9508766;
                                                                                                                                                                                                                                                                                                                                                                                                                 14007 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 28, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 CWQHISCNFPGCRTLAK 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Frank D.J., Roth M.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                   ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCL1 CAEBL
                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             elegans."
                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                         DISULPID
                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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P34611;

I ID
DIT TO DET TO DE TO DET T

NCL1_CABEL

Best Loc Matches

ò 셤 3

Gaps

28;

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Zinc-finger;
ZN FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISIONS,
                                                                                                                                                                                                                                                                                                                ZN_FING
ZN_FING
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                         ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRN_HUMAN
  ઠે
                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as along as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                         pmo1/g)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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control and exhibit seizure-like symptoms from which they eventually recover. At the highest doses tested (over 250 pmol/affect the characteristic spasmodic symptomatology, lethality occurs. Injection of a similar dose range intramuscularly into Siamese fighting fish elicited no unusual symptomatology.

-I SUBCELULIAR LOCATION: Secreted.
-I TISSUE SPECIFICITY: Expressed by the venom duct.
-I MASS SPECIFICITY: MF=2955.0; METHOD=Electrospray.
-I SIMILARITY: BELONGS TO THE P-SUPERFAMILY OF CONOTOXINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
AMIDATION (G-88 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toxin; Signal; Amidation; Vitamin K; Gamma-carboxyglutamic acid; Cleavage on pair of basic residues. SIGNAL 1 27 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90235278; PubMed=2331751;
Joho K.E., Darby M.K., Crawford B.T., Brown D.D.;
"A finger protein structurally similar to TFIIIA that binds exclusively to 58 RNA in Xenopus.";
Cell 61:293-300(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                        25.5%; Score 48; DB 1; Length 88;
45.0%; Pred. No. 8.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6C502E42A6C89E87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPASMODIC PEPTIDE TX9A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-SRP-2003 (Rel. 42, Last annotation update)
143 55 RNA binding protein (428 P43) (Thesaurin B).
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSHOKPSGCWQHISCNFPGC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF193510; AAG28406.1; -.
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87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 AA;
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P25456;
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Best Local
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P28799; P23781; P23783; P23784; Q9BWE7;
01-NOV-1991 (Rel. 20, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Granulins precursor (Acrogranin) [Contains: Paragranulin; Granulin 1 (Granulin G); Granulin 2 (Granulin F); Granulin 3 (Granulin B);
Granulin 4 (Granulin A); Granulin 5 (Granulin C); Granulin 6 (Granulin D);
GRANULIN 7 (Granulin E)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plowman G.D., Green I.M., Neubauer M.G., Buckley S.D., McDonald V.L., Todaro G.J., Shoyab M.; The epithelin precurses two proteins with opposing activities on epithelial cell growth."; Biol. Chem. 267:13073-13078(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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MEDLINE=92179253; PubMed=1542665;
MEDLINE=92179253; PubMed=1542665;
Bhandari V., Palfree R.G.E., Bateman A.;
Bhandarion and sequence of the granulin precursor cDNA from human bone marrow reveals tandem cysteine-rich granulin domains.";
Proc. Natl. Acad. Sci. U.S.A. 89:1715-1719(1992).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31
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Pred. No. 33;
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                                                                                                                                                                                                                                                                                                                                             157; ZINC_FINGER_C2H2_2; 7.
Metal-binding; RNA-binding;
15 39 C2H2-TYPE.
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                                                                                                                                 EMBL, M32473; AAA49714.1; -.
HASP, M90301; HTF3.
INTERPO: I PR007087; ZNE C2H2.
Pfam; PF00096; zf-C2H2; 9.
SMART; SM00355; ZnF C2H2; 9.
PROSITE; PS00028; ZINC FINGER C2H2 1; 7.
PROSITE; PS50157; ZINC FINGER C2H2 1; 7.
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C2H2-TYPE.
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C2H2-TYPE.
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MEDLINE=92317004; PubMed=1618805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41694 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.5%;
llarity 35.1%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251
365 AA;
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hes 13, Conserv
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                                                                                                                                         MEDLINE-2238257; PubMed-12477932;

MEDLINE-2238257; PubMed-12477932;

MEDLINE-2238257; PubMed-12477932;

MEDLINE-2238257; PubMed-12477932;

MEDLINE-2238257; PubMed-12477932;

MILAGRAR R.D., Colling F.S., Wagner L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Canainci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Nichards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Blakesley R.W., Touchman J.W., Scheurer E.D., Dickson M.C.,

A Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length

human and mouse colls sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bateman A., Belcourt D.R., Bennett H.P., Lazure C., Solomon S., "Granulins, a novel class of peptide from leukocytes."; Biochem. Biochem. Biochem. Biochem. 173:1161-1168(1990).
-!- FUNCTION: GRANULINS HAVE POSSIBLE CYTOKINE-LIKE ACTIVITY. THEY MAY PLAY A ROLE IN INFLAMMATION, WOUND REPAIR, AND TISSUE REMODELING.
-!- FUNCTION: GRANULIN A PROMOTES PROLIFERATION OF THE EPITHELIAL CELL LINE A431 IN CULTANE WHILE GRANULIN B ACTS AS AN ANTAGONIST TO GRANULIN A, INHIBITING THE GRANULIN B ACTS AS AN ANTAGONIST TO -!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note=No experimental confirmation available;
-1- TISSUE SPECIFICITY: IN MYELOGENOUS LEUKEMIC CELL LINES OF PROMONOCYTIC, PROMYELOCYTIC, AND PROBENTHROID LINEAGE, IN FIRROBLASTS, AND VERY STRONGLY IN EPITHELIAL CELL LINES. PRESENT IN INFLAMMATORY CELLS AND BONE MARROW. HIGHEST LEVELS IN KIDNEY.
                            Yu W., Gibbs R.A.; Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 206-233; 281-336; 364-396 AND 442-447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [Bold=P28799-2; Sequence=VSP_001837;
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                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS 1 AND 2)
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EMBL; X62320; CAA44196.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Leukocyte;
MEDLINE=91097544; PubMed=2268320;
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Pfam; PF00396; granulin; 7.
SMART; SM00277; GRAN; 7.
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PDB; 1G26; 01-NOV-00.
Genew; HGNC:4601; GRN.
MIM; 138945; -..
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Gaps
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(POTENTIAL).
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PROSITE; PS00799; GRANULINS; 7.
Cytokine; Repeat; Glycoprotein; Signal; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                  Score 48; DB 1; Length 593; Pred. No. 52;
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                                                                                                                                                                                                                                                                                                               /FTId=VAR 014830.
S -> H (IN REF. 6).
W -> H (IN REF. 6).
4E402BDB16DE2819 CRC64;
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                                                                                                                                                                                                       (GLCNAC
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                                                                                                                                                                                                                                                          FTId=VSP_001837
                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                             GRANULIN 1.
GRANULIN 2.
GRANULIN 3.
GRANULIN 5.
GRANULIN 6.
GRANULIN 6.
GRANULIN 7.
N-LINKED (GI
                                      POTENTIAL.
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                                                                                                                                                                                                                                                                                                                             219 219 S
386 386 W
593 AA; 63473 MW;
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45.8%;
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Query Match
Best Local Similarity 45.0.,
Local 11, Conservative
              Cytokine; Repeat; Glycoprot
Polymorphism; 3D-structure.
SIGNAL 1
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CONFLICT
SEQUENCE
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Search completed: December 12, 2003, 12:26:07 Job time : 3.06102 secs

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COMPUTER EADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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US-09-252-991A-19788
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17, Appl
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Sequence 8, Ar
Sequence 8, Ar
Sequence 8, Ar
Sequence 17, p
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Sequence 38
Sequence 4,
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Sequence 3,
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(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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(cgn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-252-91A-27618

US-09-635-872A-6

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US-09-525-991A-32591

US-09-252-991A-32591

US-09-252-991A-3264

US-09-252-991A-3264

US-09-136-769A-4

US-09-136-769A-15

US-09-136-769A-15

US-09-136-769A-15

US-09-136-769A-16

US-09-252-991A-31815

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                                                                                                                                                                                                                                                                                                                                                                                  328717 seqs, 42310858 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                               US-10-047-264A-4_COPY_67_98
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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47.5
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Sequence 19788, Application US/09252991A

Factor No. 6551795

GENERAL INFORMATION:
FACTOR OF SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPRENCE: 1071086.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

FRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 516
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US-08-727-688-25
US-08-727-688-25
; Sequence 25, Application US/08727688
; Patent No. 591938-1
; Patent No. 591938-1
; TITLE OF INVENTION:
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSES:
; ADDRESSES:
; ADDRESSES:
; ADDRESSES:
; STREET: 100 ADDOCT Park Road D377/AP6D
; CITY: ADDOCT Park
; STREET: 1L
; COUNTRY: USA
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Sequence 3, Appli
Sequence 3, Appli
Sequence 17840, A
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Pred. No. 20;
3; Mismatches 7; Indels
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                           US-09-252-991A-30903
US-09-252-991A-23454
US-09-252-991A-24354
US-08-722-001-14
US-08-722-001-14
US-08-722-001-14
US-08-722-001-14
US-08-688-415-7
US-09-688-415-7
US-09-5252-991A-18009
US-07-668-68-4
US-08-431-33-4
US-08-431-33-4
PCT-US91-02321-4
US-09-252-991A-21398
US-09-252-991A-21398
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US-09-252-991A-17840
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ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19788
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Best Local Similarity 36.6%;
Matches 15; Conservative
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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Sequence 6, Application US/09636077A

Patent No. 6537785

GENERAL INFORMATION:
APPLICATY: OWNERED, WILLIAM
ITILE OF INVENTION: METHODS OF TREATING LYSOSOMAL STORAGE DISEASE
FILE REPERENCE: 195612U50

CURRENT APPLICATION NUMBER: US/09/636,077A

CURRENT PILING DATE: 2000-08-10

PRIOR FILING DATE: 1999-09-14

NUMBER: OF SEQ ID NOS: 52

SOFTWARE: Patentin version 3.0

SEQ ID NO 6

LENGTH: 515
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Pred. No. 52;
0; Mismatches
CURRENT APPLICATION NUMBER: US/09/635,872A
CORRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/153,831
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 52
SEQ ID NO 6
LENGTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 515
TYPE: PRI
ORGANISM: HOMO Bapien8
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Best Local Similarity 56.2%; Pred. No. 3
Matches 9; Conservative 0; Mismatcl
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Sequence 30166, Application US/09252991A
Patent No. 6551795
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Best Local Similarity 56.2
Matches 9; Conservative
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LOCATION: (24)
                                                                                                                                                                                                                                                  ; NAME/KEY: SIGNAL
; LOCATION: (1)...(24)
; NAME/KEY: PROPEP
; LOCATION: (25)...(49)
US-09-635-872A-6
                                                                                                                                                                                                                                                                                                                          (25) .. (49)
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GENERAL INFORMATION:
APPLICANT: CANFIELD, WILLIAM
TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES
FILE REFERENCE: 195613USO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 26.1%; Score 49; DB Best Local Similarity 40.9%; Pred. No. 15; Matches 9; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.09-252-991A-27618
Sequence 27618, Application US/09252991A
Patent No. 6551795
                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/727,688
                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POTEMBAL, PISCILLA E.
REGISTRATION NUMBER: 33,207
TREPRENCE/DOCKET NUMBER: 5967.U/
TRLECOMMUNICATION INFORMATION:
TELEPHONE: (847) 938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 CSMKSSHQKPSGCWQHISCNFP 25
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    FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27618
                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS: LENGTH: 163 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: No. 5919638e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 36.4 Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                        CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: Bin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-727-688-25
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ORGANISM:
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DEBLICANT: MARC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32664
                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: VARIANT
LOCATION: (8)...(13)
OTHER INFORMATION: Bach Xaa is independently selected from Glu and
OTHER INFORMATION: gamma-carboxyglutamic acid, provided that at least
OTHER INFORMATION: one Xaa is gamma-carboxyglutamic acid.
NAME/KEY: VARIANT
LOCATION: (1)...(27)
OTHER INFORMATION: Xaa = Any Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.3%; Score 47.5; DB 4; Length 451; 34.6%; Pred. No. 73;
                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.0%; Score 47; DB 4; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                    14;
                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 50065/002012
CURRENT APPLICATION NUMBER: US/09/136,769A
CURRENT FILING DATE: 1998-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24_SCSVRLASARPCDC----CGVPRCR 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 SCSMKSSHQKPSGCWQHISCNFPGCR 28
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OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                  US-09-252-991A-32664
; Sequence 32664, Application US/09252991A
; Patent No. 655.795
; GENERAL INFORMATION:
                                                                                                                                         232 CHSSSSTNVPSACWRSSPGTSPTC 255
                                                                             4 CSMKSSHQKPSGCWQHISCNFPGC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09136769A
Patent No. 6307014
GENERAL INFORMATION:
APPLICANT: Furie, Bruce
APPLICANT: Furie, Brabara
APPLICANT: Righy, Alan
APPLICANT: Roepstoff, Peter
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 34.6
Matches 9; Conservative
                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-252-991A-32664
                6
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US-09-136-769A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                Matches
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## Sequence 28842. Application US/09252991A
## Pacent No. 6551795
## GENERAL INFORMATION:
## APPLICATION
## TITLE OF INVENTION:
## TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 32591, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: MAIO N. NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PAPLICATION NUMBER: US 60/074,788
PRIOR PAPLICATION NUMBER: US 60/094,190
PRIOR PLING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 162
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                                                                                                                                                                                                                                                                                                Length 365;
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Pred. No. 20;
1; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 CS-MKSSHOKPSGCWOHI-----SCNFP-GCRT 29
                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                          ; Score 48.5; DB
; Pred. No. 42;
5; Mismatches
PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILLING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 30166
                                                                                                                                                       TYPE: PRT
) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32591
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28842
                                                                                                                                                                                                                                                                                      Query Match
25.8%;
Best Local Similarity 32.4%;
Matches 12; Conservative
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Best Local Similarity 46.7%;
Matches 7; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
US-09-252-991A-32591
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Length 67;
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Patent No. 616430
GENERAL INFORMATION:
APPLICANT: Hammock, Bruce D.
APPLICANT: Moskowitz, Haim
ATITLE OF INVENTION: Insect Control With Multiple Toxins
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Majestic, Parsons, Siebert & Hsue STREET: Four Embarcadero Center, Suite 1450 CITY: San Franciso STAFF: California COUNTRY: U.S.A. ZIP: 94111-4121 COMPUTER READABLE FORM: MEDIUM TYPER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,216
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435.040
FILING DATE: 08-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 25.0%; Score 47; DB 1;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Siebert, J. Suzanne
REGISTRATION NUMBER: 28,758
REFERENCE/DOCKET NUMBER: 2500.078USO
TELECOMOUNICATION INFORMATION:
TELEPHONE: (415) 362-5556
TELEFAX: (415) 362-5418
                                                                                                                                                               2500.078US0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 KPSGCWQHISCNFPGCRTLAK 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 OPENCVYHCFPGSPGCDTLCK 29
CLASSIFICATION: 514
ATOCARETICATION: 514
ATOCARETICATION: 514
ATOCARETICATION: 514
ATOCARETICATION: 514
REGISTRATION UNDRER: 28,758
REPERENCE/DOCKET UNDRER: 2500
TELECOMMUNICATION INFORMATION: 7ELEFRAX: (415) 362-5418
TELETAX: 278638 MGPS
INFORMATION FOR SEQ ID No: 3: 5EQUENCE CHARACTERISTICS: 25EGUENCE CHARACTERISTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 278638 MGPS
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
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                                       Gaps
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Patent No. 5756340

GENERAL INFORMATION:

APPLICANT: Hamman, Rafael

APPLICANT: Hormann, Rafael

APPLICANT: Moskowitz, Haim

TITLE OF INVENTION: Insect Control With Multiple Toxins

TITLE OF INVENTION: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Majestic, Parsons, Siebert & Hsue

STREET: Four Embarcadero Center, Suite 1450

CITY: San Franciso

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: VARIANT
LOCATION: (8)...(13)
OTHER INFORMATION: Each Xaa is gamma-carboxyglutamic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 25.0%; Score 47; DB 4; Length 27; Best Local Similarity 45.0%; Pred. No. 4; Matches 9; Conservative 1; Mismatches 10; Indels
                                    Indels
                                    10;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,040
                                                                                                                                                                                                                 RESULT 11
US-09-116-769A-15
Sequence 15, Application US/09136769A
Patent No. 6307014
GENERAL INFORMATION:
APPLICANT: Furie, Barbara
APPLICANT: Furie, Barbara
APPLICANT: Rigby, Johan
APPLICANT: Roopstoff, Peter
TITLE OF INVENTION: CONOPERTIDES
FILE REFERENCE: 50055/002011
CURRENT FILING DATE: 1998-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 27
TWENT: 127
   Similarity 45.0%; Pred. No. 4; 9; Conservative 1; 'Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT
LOCATION: (1)...(27)
OTHER INFORMATION: Xaa = Any Amino Acid
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i LOCATION: (1)...(27)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-136-769A-15
                                                                                                27
                                                                                                                                     4 NSCQXHSDCXSHCICTFRGC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 SSHOKPSGCWQHISCNFPGC 27
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                                                                                             8 SSHOKPSGCWQHISCNFPGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Conus textile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 94111-4121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-435-040-3
Best Local
Matches
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Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR SEQ ID NOS: 33142
SEQ ID NO 25235
LENGTH: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFREENCE: 107196.136
CURRENT APPLICATION NUMBER: US,60/02/22,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US,60/074,788
PRIOR APPLICATION NUMBER: US,60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 144
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7
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                                                                                                                  Score 47; DB 3; Length 67; Pred. No. 11; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                            RESULT 14
US-09-252-991A-31815
; Sequence 31815, Application US/09252991A
; Patent No. 6551755.
                                                                                                                                                                                                                       12 KPSGCWQHISCNFPGCRTLAK 32
                                                                                                                                                                                                                                                      9 QPENCVYHCFPGSPGCDTLCK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31815
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US-09-252-991A-25235
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                                                                                                                    Query Match
Best Local Similarity 42.9%;
Matches 9; Conservative
                    ; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-09-020-216-3
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Best Local Similarity
Matches 10, Conserve
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HYPOTHETICAL:
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140 SWSNNSPHRKAITTLTPAACWITGWRSSPMRSSCGSPICCPLA 182
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Search completed: December 12, 2003, 12:16:33 Job time : 4.14576 secs

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hypothetical prote
CO275.9 protein -
probable retroelem
hypothetical prote
probable retroelem
hypothetical prote
probable retroelem
CD59 protein - bab
CD59 protein - gre
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gammma-crystallin
extracellular matr
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                             1 MFSCSMKSSHQKPSGCWQHISCNFPGCRTLAK 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283308 seqs, 96168682 residues
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                                                                                                               OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1709052
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CYRTG1
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CYMSG3
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A70645
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Match Length
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
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E64024 181940 181940 181940 181930 181930 191955 101955 101955 101955 101955 101955 101911 102916 102916 102916	ALIGNMENTS (fragment) no, M.T.; Faras, A.J. 92 nous sequences related t MUID:92194452; PMID:154 slated from GB/EMBL/DDBJ 46; NID:9181990; PID:955	re 59.5; d. No. 0.4 Mismatches 30	an r, P.A.; K n-based si 98207242; from GB/F i NID:g304 e: brain;
00000000000000000000000000000000000000	(fragmul) se_rev, M. 12 12 12 12 12 12 13 14 16 16 17 18 18 18 18 18 18 18 18 18 18 18 18 18	S%; S%; NPPG NPPG	human Lrevis Slder, Ttion- JD:98 Tted f
63 325 325 325 325 325 527 680 491 491 1241 1303	human (fragmiens (man) #sequence_rev. ree-Jacino, M.7179, 1992 and 156825; MUD: Y; translated http://doi.org/	S - Ka	DBCCR1 - hum ns (man) sequence_rev be, M.; Elde 1999 d methylatio 16537; MUID: ; translated Bb; MBL:AF027734 : tissue typ q33 hypothetical
22 22 22 22 22 22 22 22 22 22 22 22 22	bin - hu 396 #sapient 396 #sapient 320 #sapient 1800 #sapient 1810 #sapient	Similarity 52.2%; Pre 2; Conservative 0; QKPSGCWQHISCNFPGGRILL	sapiens sapiens 059 #se 059 #se 059 #se maccomber: 216 052 inary; inary; inary; inary; inary; inary; inary; ores: EMBo ource: 9q32-q3
44444444444444444444444444444444444444	1. Protein series appleance of the protein series se	atch cal S 12 11	cal pro i: Homo i: Homo con: T09 48., T ; I 48., T ; I 28. T09 con: T09 prelim e type: eferenc
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Gaps

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Score 55; DB 2; Length 761; Pred. No. 18; 5; Mismatches 5; Indels

29.3%;

Query Match 29.3 Best Local Similarity 50.0 Matches 10, Conservative

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A,Molecule type: protein
A,Residues: 1-173 <MH>>
R;Chiou, S.H.; Azari, P.; Himmel, M.E.
J. Protein Chem. 7, 67-80, 1988
A;Title: Physicochemical characterization of gamma-crystallins from bovine lens-hydrody
A;Reference number: A60890; MUID:89351571; PMID:3255364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Breitman, M.L.; Lok, S.; Wistow, G.; Piatigorsky, J.; Treton, J.A.; Gold, R.J.M.; Tsn Proc. Natl. Acad. Sci. U.S.A. 81, 7762-7766, 1984
A;Title: gamma-crystallin family of the mous lens: structural and evolutionary relation A;Reference number: A94021; MUID:85088487; PMID:6096855
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C;Comment: There are at least seven different gamma crystallins identified in mouse les
C;Superfamily: beta-crystallin
C;Keywords: duplication; eye lens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: protein
A,Residues: 1-25 cCHI>
A,Note: 14-His, 15-Krg, 22-Cys, 23-Pro, and 24-Asp were also found and may indicate
C.Superfamily: beta-crystallin
C,Keywords: duplication; eye lens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: S04266; C60890
R;White, H.E., Driessen, H.P.C.; Slingsby, C.; Moss, D.S.; Lindley, P.F.
J. Mol. Biol. 207, 217-235, 1989
A;Title: Packing interactions in the eye-lens. Structural analysis, internal A;Reference number: S04265; MUID:89293855; PMID:2738925
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C.Species: Mus musculus (house mouse)
C.Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 22-Jun-1999
A; Residues: 1-173 cMOO>
A; Residues: 1-173 cMOO>
A; Cross-references: GB:J00716; NID:g203634; PIDN:AAA40987.1; PID:g203635
C; Superfamily: beta-revystallin
C; Keywords: duplication; eye lens
F; 1-39/Domain: crystallin repeat cGKL>
F; 40-82/Domain: crystallin repeat cGK2>
F; 87-127/Domain: crystallin repeat cGK3>
F; 128-167/Domain: crystallin repeat cGK3>
                                                                                                                                                                                                                                                                                                                                          Length 173;
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                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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Pred. No. 17;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                          Score 51; DB Pred. No. 17; 5; Mismatches
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F:41-83/Domain: crystallin repeat <GK2>
F:88-128/Domain: crystallin repeat <GK3>
                                                                                                                                                                                                                                                                                                                                          27.1%;
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Best Local Similarity 30.8
Matches 12; Conservative
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Best Local Similarity
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A; Residues: 1-174 <BRE>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 149617
R;Lok, S:; Breitman, M.L.; Chepelinsky, A.B.; Piatigorsky, J.; Gold, R.J.; Tsui, L.C.
Mol. Cell. Biol. 5, 2221-2310, 1985
A;Title: Lens-specific.promoter activity of a mouse gamma-crystallin gene.
A;Reference number: 149617; MUID:86284663; PMID:3837188
A;Recession: 149617
A;Accession: 149617
A;Accession: 149617
A;Accession: 149617
A;Coss-references: GB:M11039; NID:g192784; PIDN:AAA03227.1; PID:g192785
A;Cross-references: GB:M11039; NID:g192784; PIDN:AAA03227.1; PID:g192785
C;Genetics: A;Introns: 3/3
C;Superfamily: beta-crystallin
C;Keywords: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gamma-F-crystallin - mouse (fragment)
(Species: Mus musculus (house mouse)
(Cipercies: Mus musculus (house mouse)
(Cipercies: Mus musculus (house mouse)
(Cipercies: Musculus)
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C;Species: Rattus norregicus (Norway rat)
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 22-Jun-1999
C;Accession: A02930
R;Moormann, R.J.M.; den Dunnen, J.T.; Bloemendal, H.; Schoenmakers, J.G.G.
Proc. Natl. Acad. Sci. U.S.A. 79, 6876-6880, 1982
A;Title: Extensive intragenic sequence homology in two distinct rat lens gamma-crystalli
A;Reference number: A93934; MUID:83091061; PMID:6294661
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A;Molecule type: mRNA
A;Residues: 1-159 <RES>
A;Cross-references: GB:M64543; NID:g192788; PIDN:AAA53525.1; PID:g567200
C;Superfamily: beta-crystallin
C;Keywords: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 51; DB 2; Length 69;
Pred. No. 7.6;
5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 FSCSMKSSHQKP-----SGCWQ-HISCNFPGCR 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 FSCSMKSSHQKP-----SGCWQ-HISCNFPGCR 28
       24
                                                   19 SVQPSHQEPAGTDQHVSKEF 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.1%;
30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 30.87
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hes 12; Conserva
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C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Nov-1997
R;Graw, J: NoSession: 180596; S18835.
R;Graw, J: Coban, L.; Liebstein, A.; Werner, T.
Gene.104, 265-270, 1991
A;Title: Murine gamma E-crystallin is distinct from murine gamma 2-crystallin.
A;Reference number: J80596; MUID:9209923; PMID:1916296
A;Accession: J80596; MUID:9209923; PMID:1916296
A;Accession: J70596
A;Accession: J80596
A;Accession: J80596
A;Accession: J80596
A;Accession: J80596
A;Accession: J80596
A;Grestios: EMBL:X57855
A;Grestios: A;Gene: gamma-E-cry
A;Introns: J8, J8, 484
A;Gene: gamma-E-cry
A;Introns: J8, J8, 484
C;Superfamily: beta-crystallin
C;Keywords: duplication
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NiAlbernate names: gamma-D-crystallin
CiSpecies: Rattus norvegicus (Norway rat)
CiSpecies: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 13-Aug-1999
CiAccession: D24060; 183433; 560744
Siden Dunnen, J.T.; Moormann, R.J.M.; Lubsen, N.H.; Schoenmakers, J.G.G.
J. Mol. B101. 189, 37-46, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 51; DB 2; Length 174; Pred. No. 17; 5; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 YECSTDHSNLQPYFSRCNSVRVDSGCWMLYEQPNFTGCQ 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 FSCSMKSSHQKP-----SGCWQ-HISCNFPGCR 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 YECSTDHSNLQPYFSRCNSVRVDSGCWMLYEQPNFTGCQ 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.1%;
30.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 27.1
Best Local Similarity 30.8
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 FSCSMKSSHQKP----
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Matches 12; Conservative
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A;Residues: 1-174 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A02932
R;Breitman, M.L.; Lok, S.; Wistow, G.; Piatigorsky, J.; Treton, J.A.; Gold, R.J.M.; Tsui
R;Breitman, M.L.; Lok, S.; Wistow, G.; Piatigorsky, J.; Treton, J.A.; Gold, R.J.M.; Tsui
A;Title: gamma-crystallin family of the mous lens: structural and evolutionary relations
A;Reference number: A94021; MUID:85088487; PMID:6096855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: GB:K02583; NID:g192778; PIDN:AAA37475.1; PID:g309197
Comment: There are at least seven different gamma crystallins identified in mouse lens
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C;Species: Mus musculus (house mouse)
C;Accession: S26811
R;Werner, T.
submitted to the EMBL Data Library, February 1991
A;Reference number: S26811
                                                                                                           Gaps
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                         Ouery Match 27.1%; Score 51; DB 1; Length 174; Best Local Similarity 30.8%; Pred. No. 17; Matches 12; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.1%; Score 51; DB 1; Length 174; 30.8%; Pred. No. 17; Ative 5; Mismatches 10; Indels
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                                                                                                                                                                  2 FSCSMKSSHQKP-----SGCWQ-HISCNFPGCR 28
                                                                                                                                                                                                                   17 YECSTDHSNLQPYFSRCNSVRVDSGCWMLYEQPNFTGCQ 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gamma-B-crystallin - mouse
C;Species: Mus musculus (house mouse)
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C;Superfamily: beta-crystallin
C;Keywords: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 30.88
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Molecule type: mRNA
A, Residues: 1-174 <BRE>
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A,Molecule type: DNA
A,Residues: 1-174 <WER>
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RESULT 9

ઠ 요 RESULT 10

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Rivan Es, S.; Nieuwenhuijsen, B.W.; Lenouvel, F.; van Deursen, E.M.; Schaap, submitted to the EMBL Data Library, April 1994
A;Description: Universal signals control slime mold stalk information.
A;Reference number: S44208
A;Accession: S44208
A;Accession: S4208
A;Residues: 1-313 <-VAM>A;Cross-references: EMBL:X78948; NID:g474918; PIDN:CAA55545.1; PID:g474919
                                                                                                                                                                              extracellular matrix protein B - Dictyostelium minutum (fragment)
C;Species: Dictyostellum minutum
C;Date: 07-0ct-1994 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C;Accession: S44208
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26.9%; Score 50.5; DB 2; Length 313;
Best Local Similarity 48.1%; Pred. No. 32;
Matches 13; Conservative 1; Mismatches 10; Indels
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26.6%; Score 50; DB 2; Length 467;
Best Local Similarity 52.9%; Pred. No. 53;
Matches 9; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-467 <BEV>
A;Cross-references: EMBL:AL021712
A;Experimental source: cultivar Columbia; BAC clone T10114
      17 YECSTDHSNLQPYFSRCNSVRVDSGCWMLYEQPNFTGCQ 55
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A;Introns: 39/3; 75/1; 334/3; 383/3
A;Note: T10114 110
C;Superfamil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Introns: 24/1
C;Keywords: extracellular matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
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A; Fitle: Concerted and divergent evolution within the rat gamma-crystallin gene family. A; Reference number: A92927; MUD:87060933; PMID:3783678
A; Accession: D24060
A; Molecule type: DNA
A; Residues: 1-174 cAEN.
A; Residues: 1-174 cAEN.
A; Cross-references: GB: M19359; NID:9203626; PIDN:AA440984.1; PID:9203630; GB:M19354; GB: R; Den Dunnen, J.T.; van Neck, J.W.; Cremers, F.P.M.; Lubsen, N.H.; Schoenmakers, J.G.G.
A; Title: Nucleotide sequence of the rat gamma-crystallin gene region and comparison with A; Reference number: 160312; MUD:87477; PMID:2777080
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C;Accession: 156381; 183434
C;Accession: 156381; 183434
C;Accession: 156381; Janunen, J.T.; Mulleners, L.; Andreoli, P.; Bloemendal, H.; Schoenm J. Mol. Biol. 171, 35-368, 1983
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
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A;Cross-references: EMBL:X00271; NID:956193; PIDN:CAA25073.1; PID:9295917
A;Cross-references: EMBL:X00271; NID:956193; P.P.M.; Lubsen, N.H.; Schoenmakers, J.G.G.
Gene 78, 201-213, 1989
A;Title: Nucleotide sequence of the rat gamma-crystallin gene region and comparison with A;Reference number: I60312; MUID:89378747; PMID:2777080
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A,Rolecule type: DNA
A,Rolecule type: DNA
A,Residues: 1-174 <RES>
A,Cross-references: GB:M19359; NID:g203626; PIDN:AAA40984.1; PID:g203630
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A,Title: High level expression of rat gamma-D-crystallin in Escherichia coli.
A,Reference number: S60744; MUID:95151850; PMID:7849105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Status: preliminary
A,Modecule type: mRNA
A,Residues: 1-174 <000x
A,Cross-references: EMBL:X57169; NID:g929827; PIDN:CAA40458.1; PID:g929828
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AjStatus: prelimary; translated from GB/EMBL/DDBJ
AjOlecule type: DNA
AjResiduse: 1-174 cRE2>
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Pred. No. 17;
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N;Alternate names: gamma-E-crystallin
C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Genetics: A,Introns: 3/3; 84/3
C,Superfamily: beta-crystallin
C,Keywords: duplication
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Best Local Similarity 30.8%
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C, Superfamily: beta-crystallin
C, Keywords: duplication
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